



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:18 PM UTC

PDB ID : 6OGI / pdb_00006ogi
EMDB ID : EMD-20058
Title : 70S termination complex with RF2 bound to the UAG codon. Rotated ribosome conformation (Structure V)
Authors : Svidritskiy, E.; Demo, G.; Loveland, A.B.; Xu, C.; Korostelev, A.A.
Deposited on : 2019-04-02
Resolution : 3.40 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:

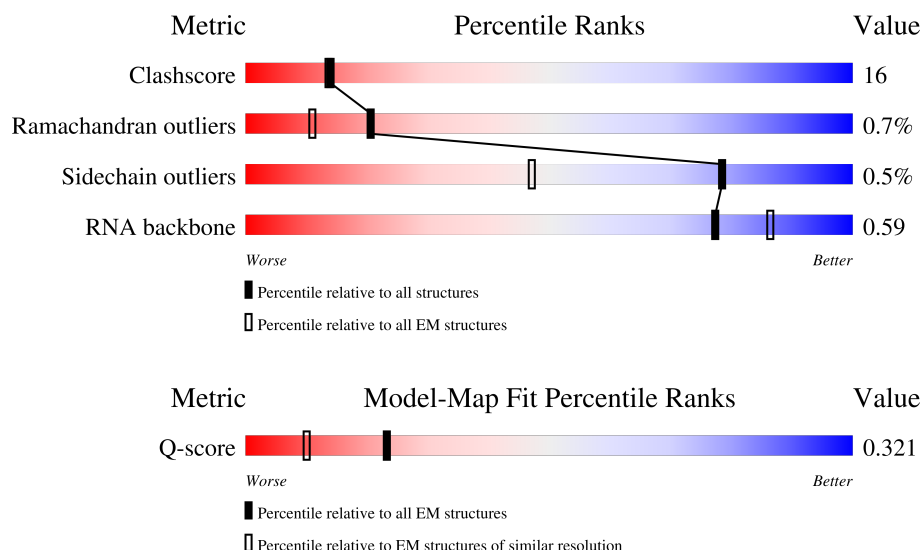
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



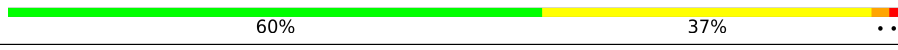
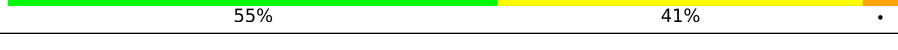
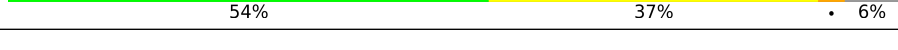
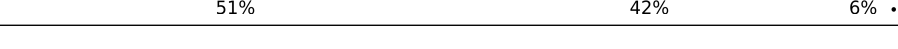
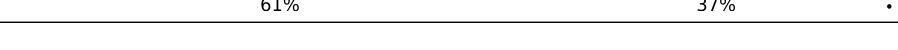
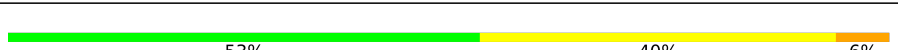
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	b	273	
2	c	209	
3	d	201	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	e	179	
5	f	177	
6	g	149	
7	j	142	
8	k	123	
9	l	144	
10	m	136	
11	n	127	
12	o	117	
13	p	115	
14	q	118	
15	r	103	
16	s	110	
17	t	100	
18	u	104	
19	v	94	
20	w	85	
21	x	78	
22	y	63	
23	z	59	
24	B	57	
25	C	55	
26	D	46	
27	E	65	
28	F	38	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	G	241	
30	H	233	
31	I	206	
32	J	167	
33	K	131	
34	L	156	
35	M	130	
36	N	130	
37	O	103	
38	P	129	
39	Q	124	
40	R	118	
41	S	101	
42	T	89	
43	U	82	
44	V	84	
45	W	75	
46	X	92	
47	Y	87	
48	Z	71	
49	a	234	
50	3	1539	
51	1	2903	
52	2	120	
53	5	77	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	4	27	19%15%48%11%26%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 144895 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 8 is a protein called 50S ribosomal protein L14.

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

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 10 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 12 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 13 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 14 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 15 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 16 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 18 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	u	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 19 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 20 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 24 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 25 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	C	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 26 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 27 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 29 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

- Molecule 30 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 31 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 32 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 33 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	101	Total	C	N	O	S	0	0
			824	520	149	149	6		

- Molecule 34 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 35 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 36 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 37 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 38 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 39 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 40 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 41 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 42 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 43 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 44 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 45 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 46 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 47 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 49 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	a	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 50 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1036415628

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

- Molecule 53 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	74	Total	C	N	O	P	0	0
			1578	704	286	515	73		

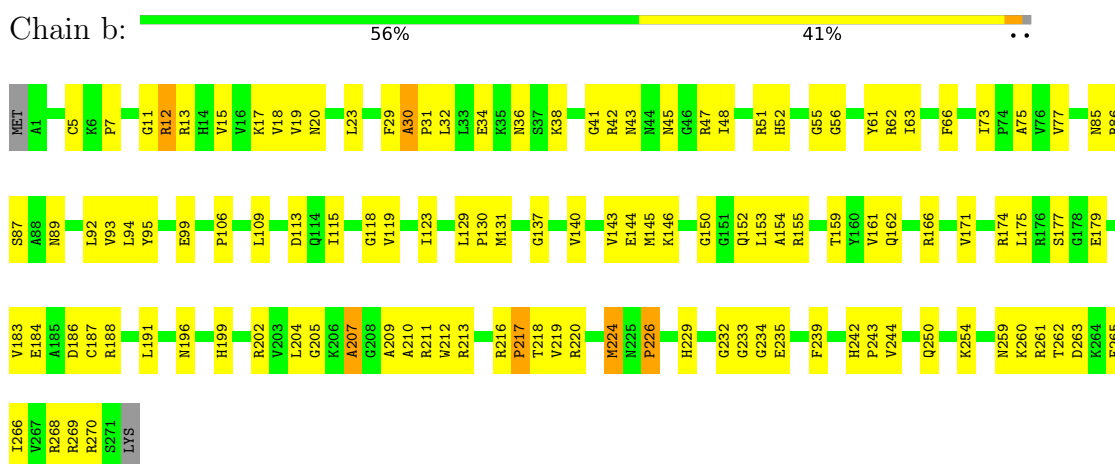
- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	20	Total	C	N	O	P	0	0
			437	197	91	130	19		

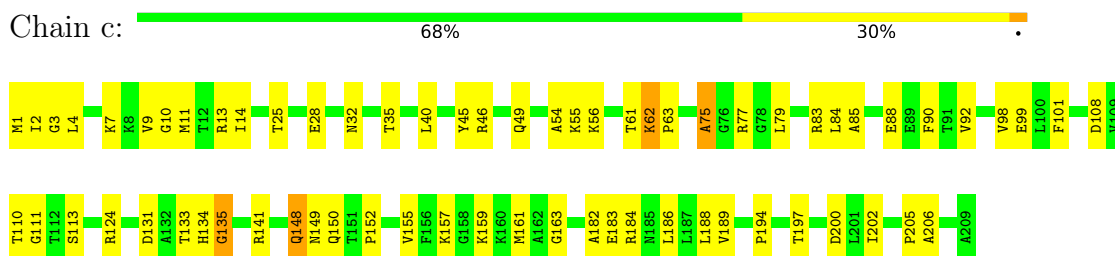
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

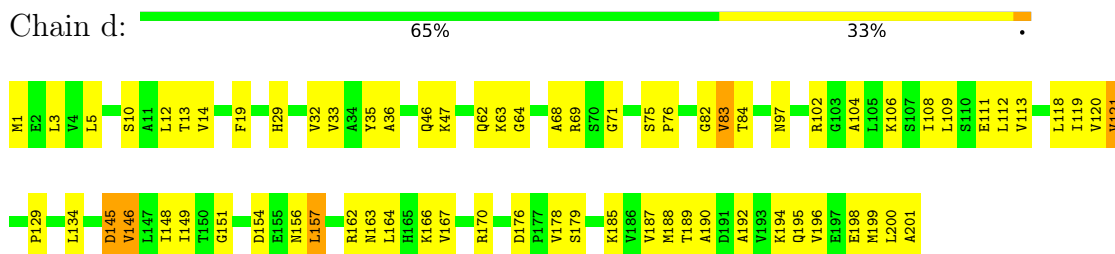
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

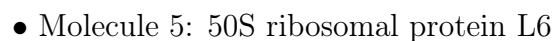


- Molecule 3: 50S ribosomal protein L4

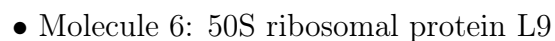


- Molecule 4: 50S ribosomal protein L5

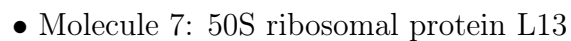
Frequency	Percentage
Daily	34%
Weekly	54%
Monthly	11%



Government	Percentage
Current government	14%
Opposition	58%
Current government	38%



Government	Percentage
Current government	60%
Previous government	44%
Previous government's predecessor	10%



Response	Percentage
Doing a good job	60%
Not doing a good job	37%
Don't know	3%



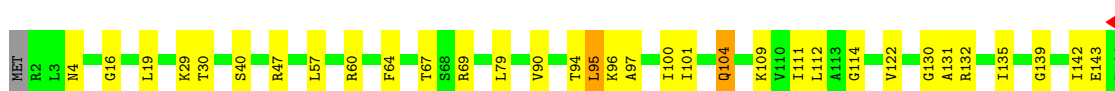
• Molecule 8: 50S ribosomal protein L14

Chain k: 54% 42% ..



• Molecule 9: 50S ribosomal protein L15

Chain l: 76% 22% ..



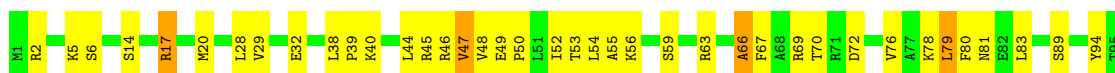
• Molecule 10: 50S ribosomal protein L16

Chain m: 55% 41% .



• Molecule 11: 50S ribosomal protein L17

Chain n: 54% 37% 6%



• Molecule 12: 50S ribosomal protein L18

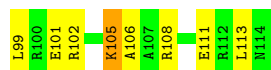
Chain o: 51% 42% 6%





- Molecule 13: 50S ribosomal protein L19

Chain p: 61% 37% ..



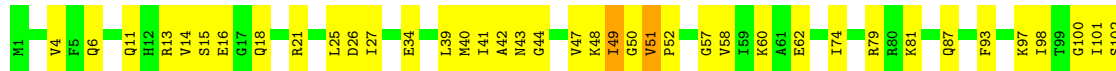
- Molecule 14: 50S ribosomal protein L20

Chain q: 56% 42% ..



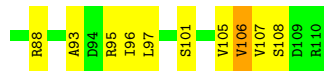
- Molecule 15: 50S ribosomal protein L21

Chain r: 62% 36% .



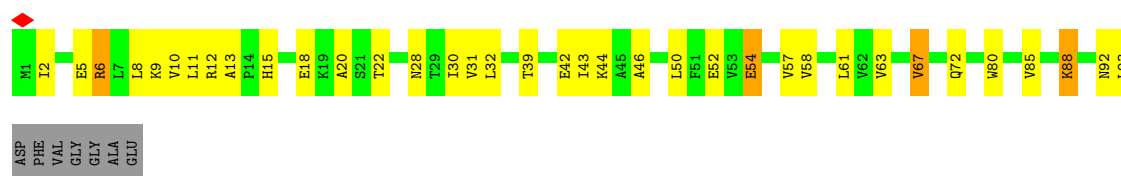
- Molecule 16: 50S ribosomal protein L22

Chain s: 57% 39% .

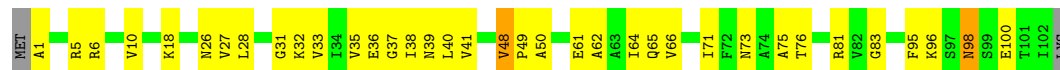


- Molecule 17: 50S ribosomal protein L23

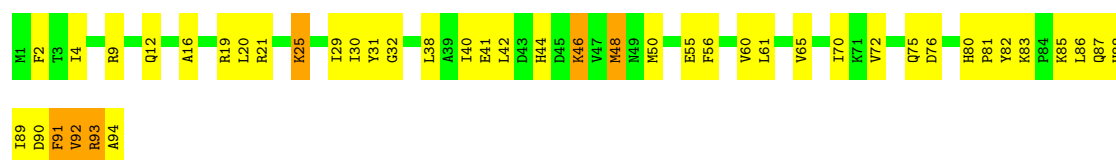
Chain t: 57% 32% 7%



• Molecule 18: 50S ribosomal protein L24



• Molecule 19: 50S ribosomal protein L25



• Molecule 20: 50S ribosomal protein L27



• Molecule 21: 50S ribosomal protein L28



• Molecule 22: 50S ribosomal protein L29



• Molecule 23: 50S ribosomal protein L30





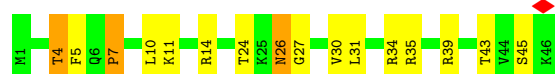
- Molecule 24: 50S ribosomal protein L32



- Molecule 25: 50S ribosomal protein L33



- Molecule 26: 50S ribosomal protein L34



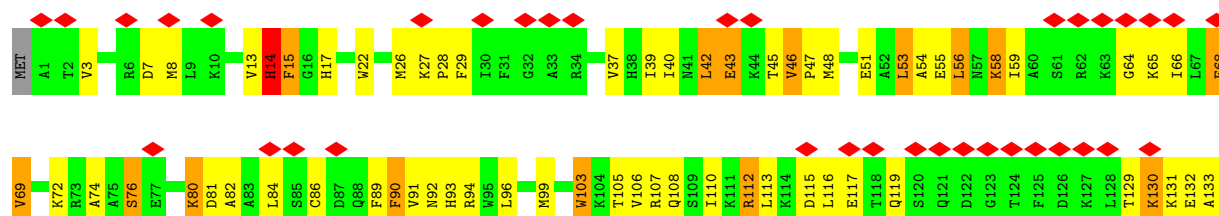
- Molecule 27: 50S ribosomal protein L35

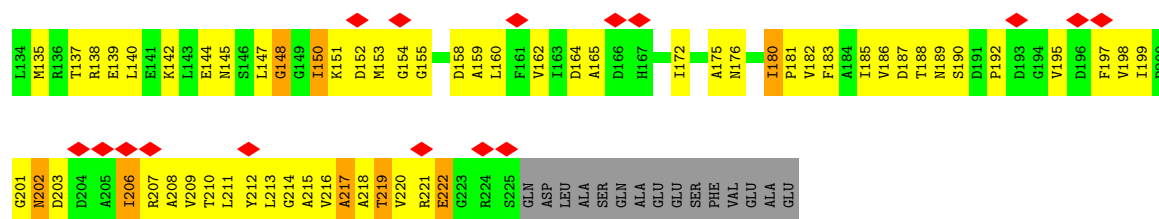


- Molecule 28: 50S ribosomal protein L36

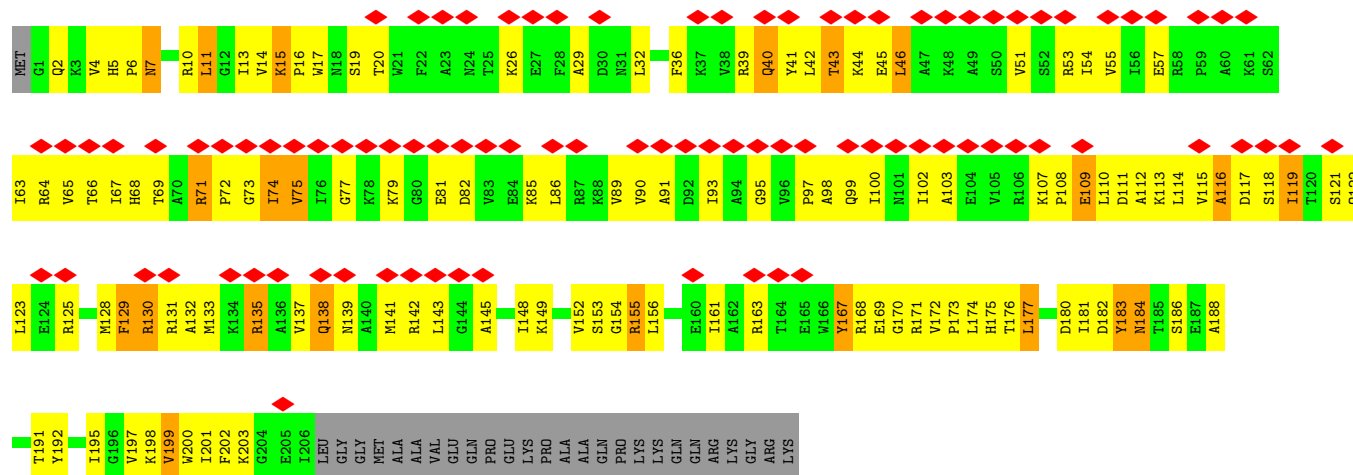


- Molecule 29: 30S ribosomal protein S2

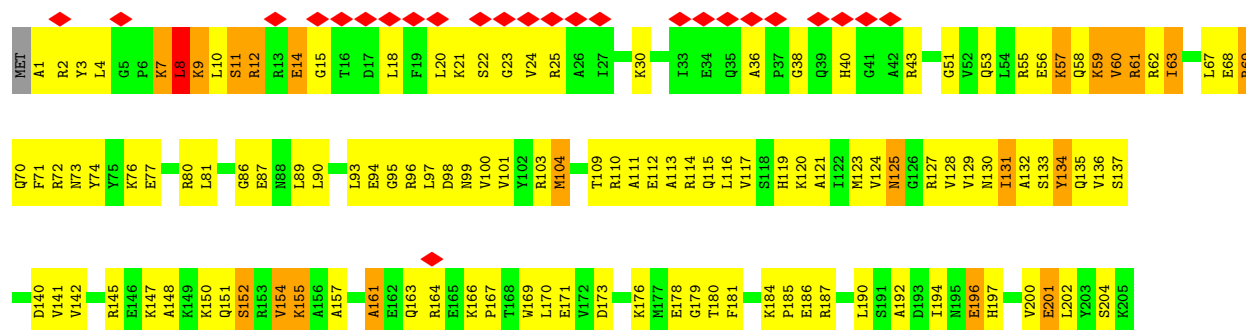




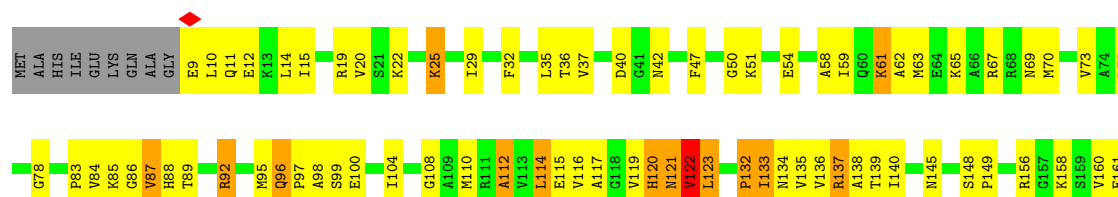
• Molecule 30: 30S ribosomal protein S3



• Molecule 31: 30S ribosomal protein S4

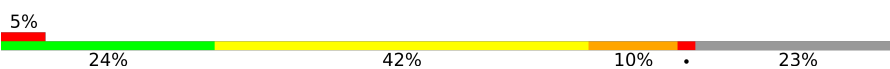


• Molecule 32: 30S ribosomal protein S5



E162
I163
L164
G165
LVS

• Molecule 33: 30S ribosomal protein S6

Chain K: 

M1 R2 R3 Y4 E5 I6 V7 F8 M9 E10 H11 P12 D13 Q14 S15 E16 Q17 V18 P19 G20 G21 M21 E22 E23 R24 Y25 T26 A27 A28 I29 T30 G31 A32

F67 Q68 E69 I70 I71 L74 E75 T76 R79 P80 N81 D82 A83 Q17 V84 I85 S86 S87 M88 E89 M90 R91 T92 K93 H94 A95 G96 T97 E98 A99 S100 P101 MET VAL LYS ALA LYS ASP GLU ARG ARG ARG ARG ASP PHE ALA ASN GLU THR ALA ASP ASP ALA GLY

ASP
SER
GLU

• Molecule 34: 30S ribosomal protein S7

Chain L: 

MET P1 R2 R3 R4 V5 I6 G7 Q8 R9 K10 I11 L12 P13 D14 P15 K16 F17 G18 S19 E20 L21 L22 A23 K24 N27 I28 L29 M30 V31 D32 G33 K34 K35 S36 T37 A38 A39 S40 I41 V42 Y43 S44 A45 E47 T48 L49 A50 Q51 R52 S53 G54 K55 S56 E57 L58 E59 A60

F61 E62 V63 A64 L65 E66 M67 V68 R69 P70 T71 V72 E73 V74 K75 S76 R77 R78 G80 G81 S82 T83 Y84 Q85 V86 P87 E88 E89 V90 R91 P92 V93 R94 R95 N96 A97 L98 A99 M100 R101 W102 I103 V104 E105 A106 A107 R108 K109 G110 D112 K113 S114 M115 A116 L117 R118 L119 A120

N121 E122 L123 S124 D125 A126 A127 N128 K129 V130 T132 A133 V134 K135 K136 E137 E138 D139 V140 H141 H142 M143 A144 E145 A146 N147 K148 A149 F150 A151 HIS TYR ARG TRP

• Molecule 35: 30S ribosomal protein S8

Chain M: 

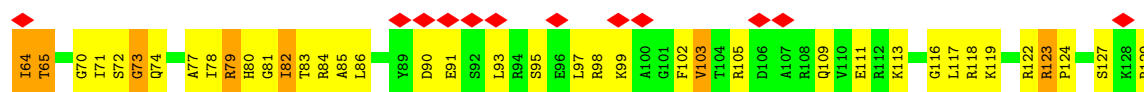
MET S1 S2 Q3 S124 D125 A126 A127 N128 K129 V130 T132 A133 V134 K135 K136 E137 E138 D139 V140 H141 H142 M143 A144 E145 A146 N147 K148 A149 F150 A151 HIS TYR ARG TRP

M95 L98 G99 I100 A101 V102 A114 A115 R116 Q117 A118 G119 L120 G121 G122 I124 C126 A129

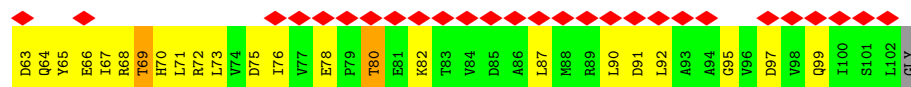
• Molecule 36: 30S ribosomal protein S9

Chain N: 

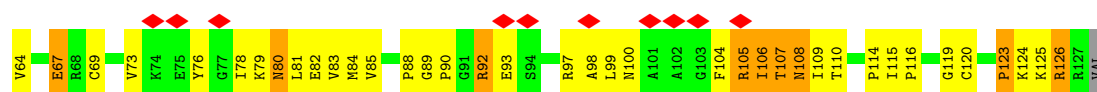
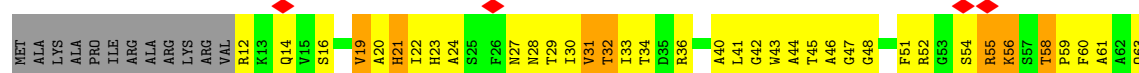
MET ALA GLU N3 Q4 T5 Y6 R10 R11 K12 A15 A16 R17 R18 V19 I20 K21 P22 G23 G24 G25 K26 I27 V28 I29 N30 Q31 R32 S33 L34 E35 Q36 T37 F38 G39 R40 E41 T42 A43 V46 V47 R48 Q49 P50 L51 E52 L53 V54 D55 H56 V57 E58 K59 D61 L62 V63



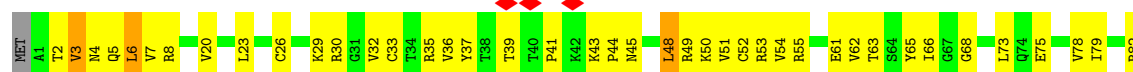
• Molecule 37: 30S ribosomal protein S10



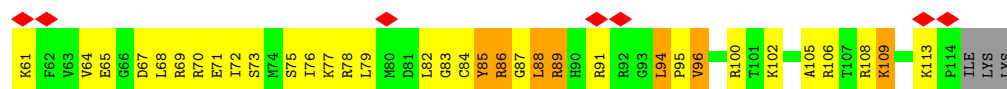
• Molecule 38: 30S ribosomal protein S11



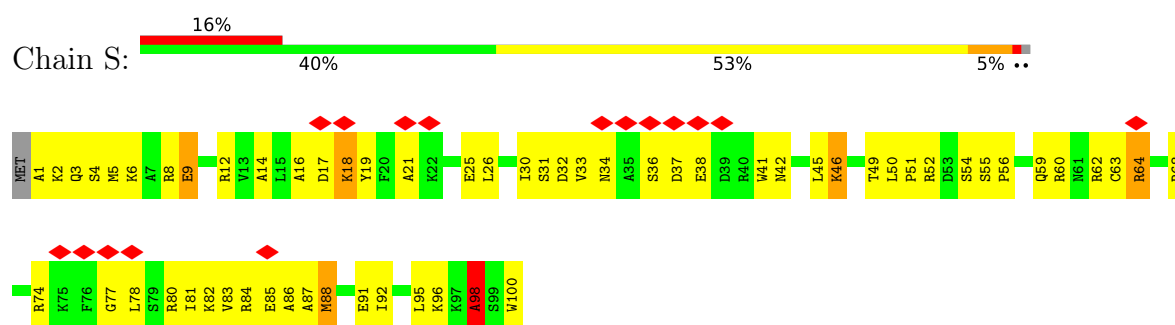
• Molecule 39: 30S ribosomal protein S12



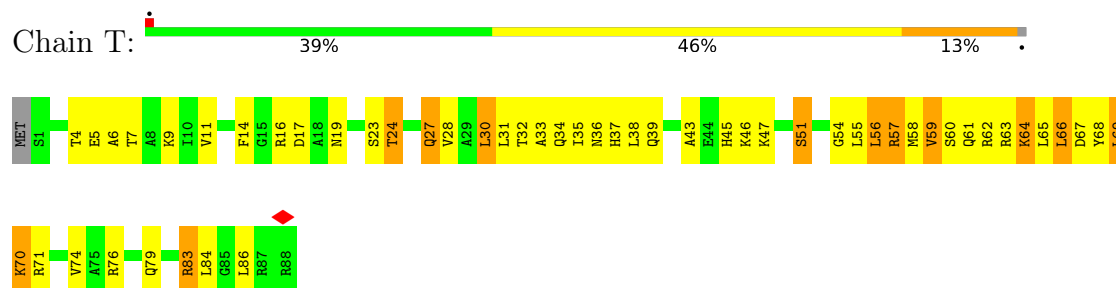
• Molecule 40: 30S ribosomal protein S13



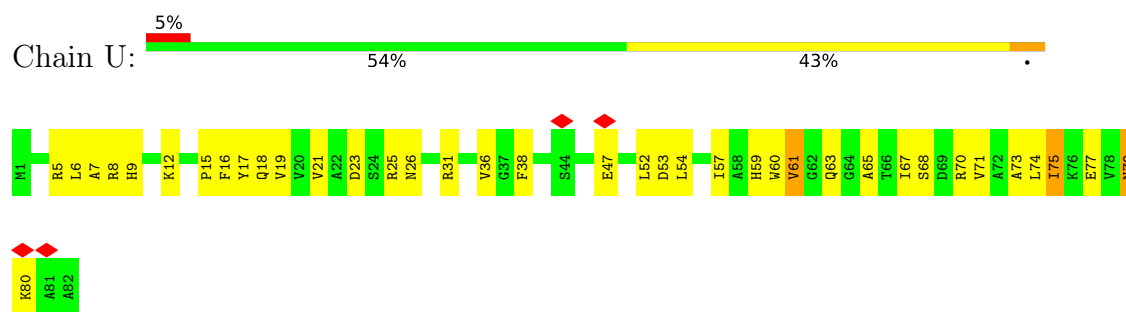
• Molecule 41: 30S ribosomal protein S14



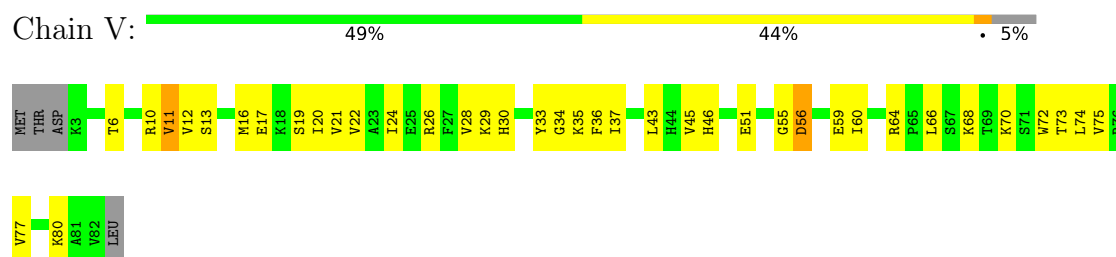
- Molecule 42: 30S ribosomal protein S15



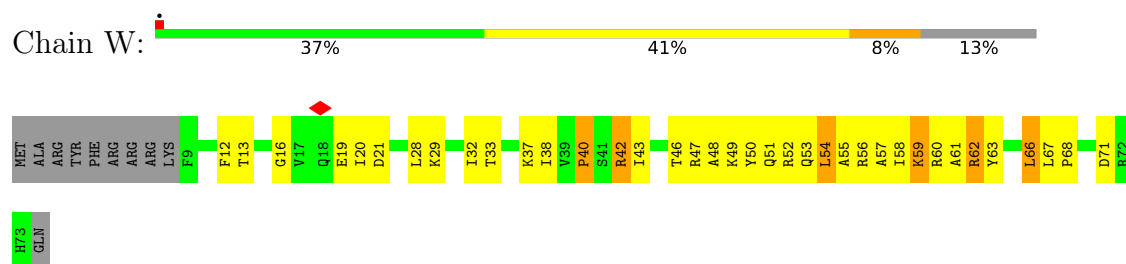
- Molecule 43: 30S ribosomal protein S16



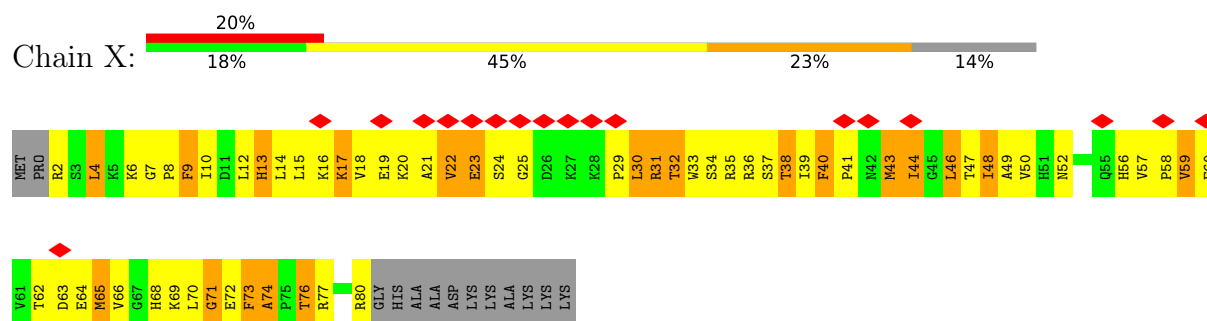
- Molecule 44: 30S ribosomal protein S17



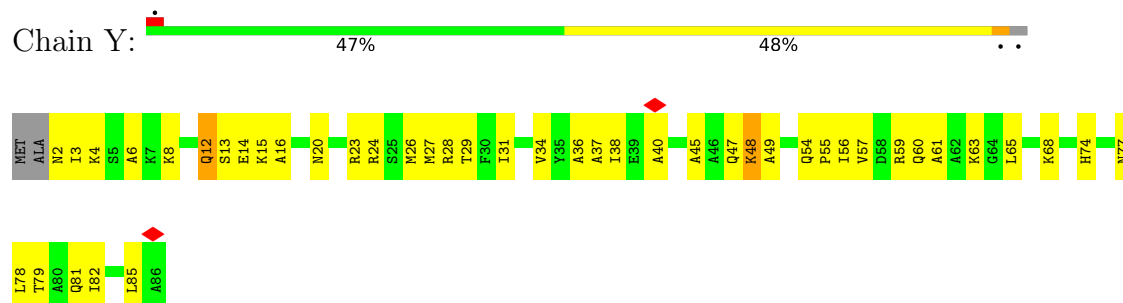
- Molecule 45: 30S ribosomal protein S18



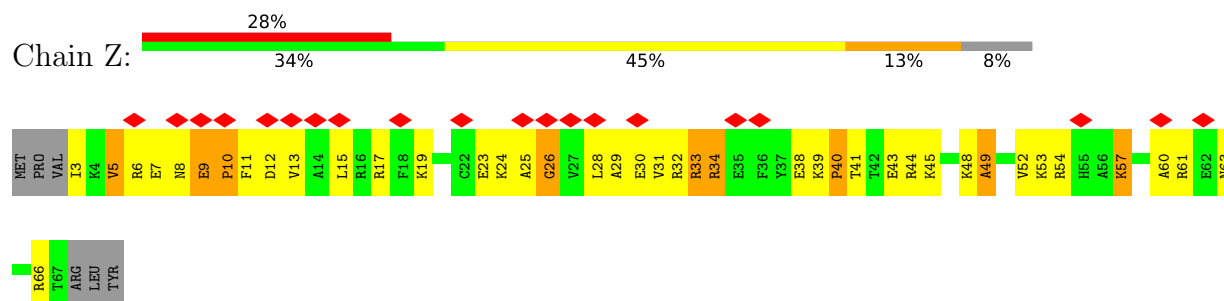
- Molecule 46: 30S ribosomal protein S19



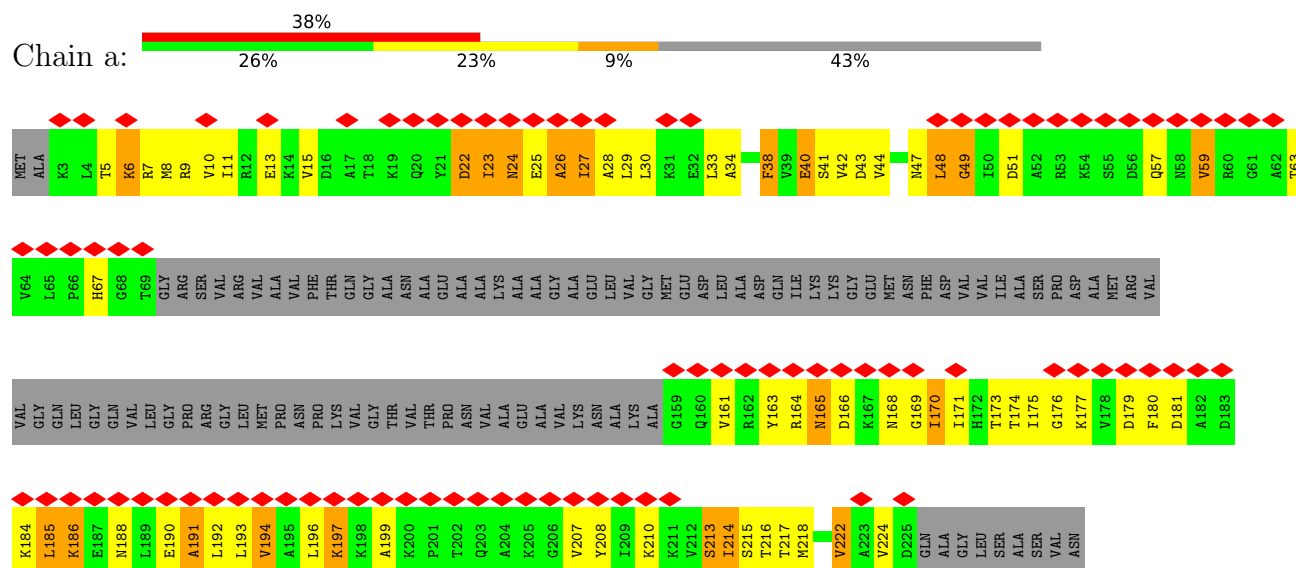
- Molecule 47: 30S ribosomal protein S20



- Molecule 48: 30S ribosomal protein S21

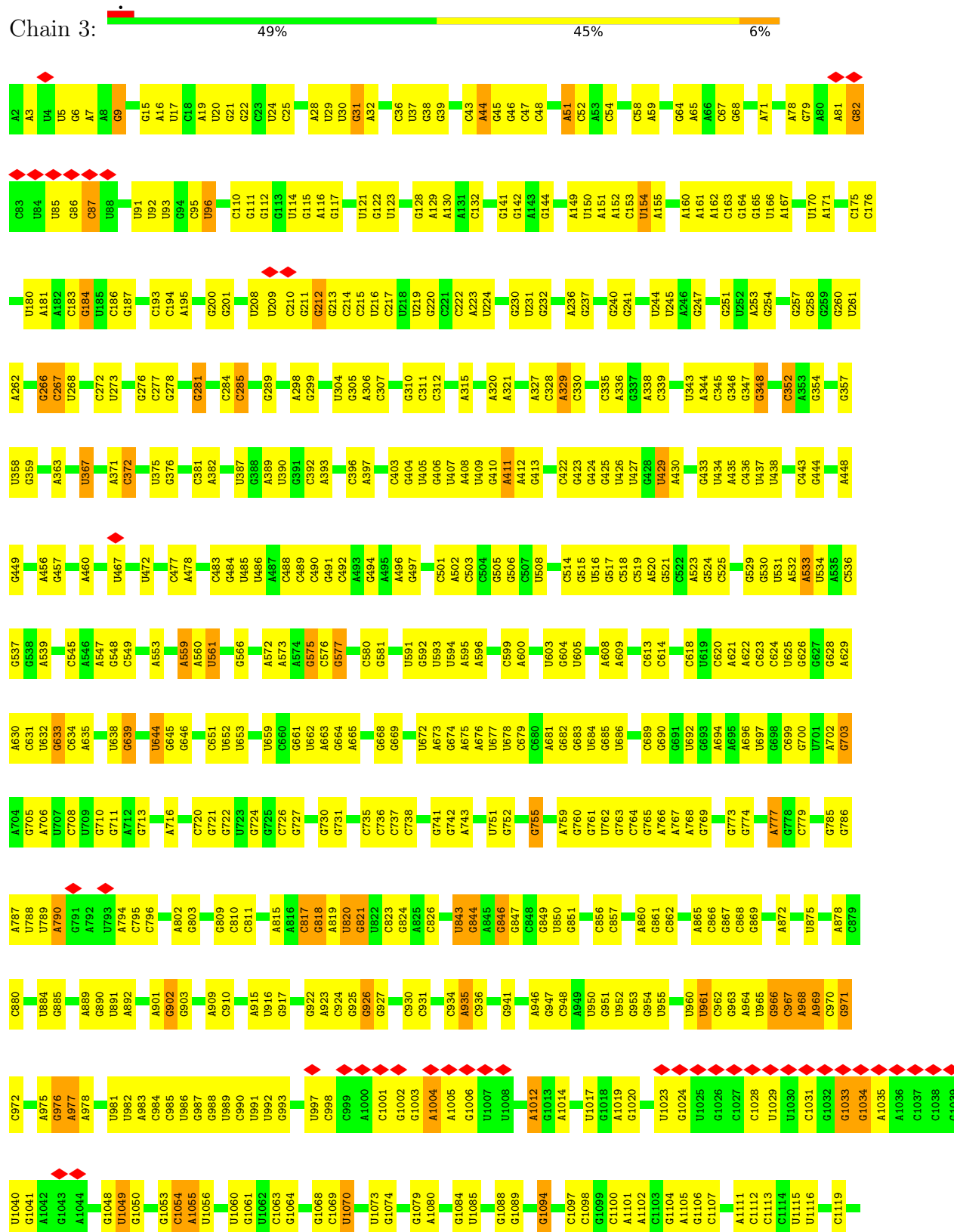


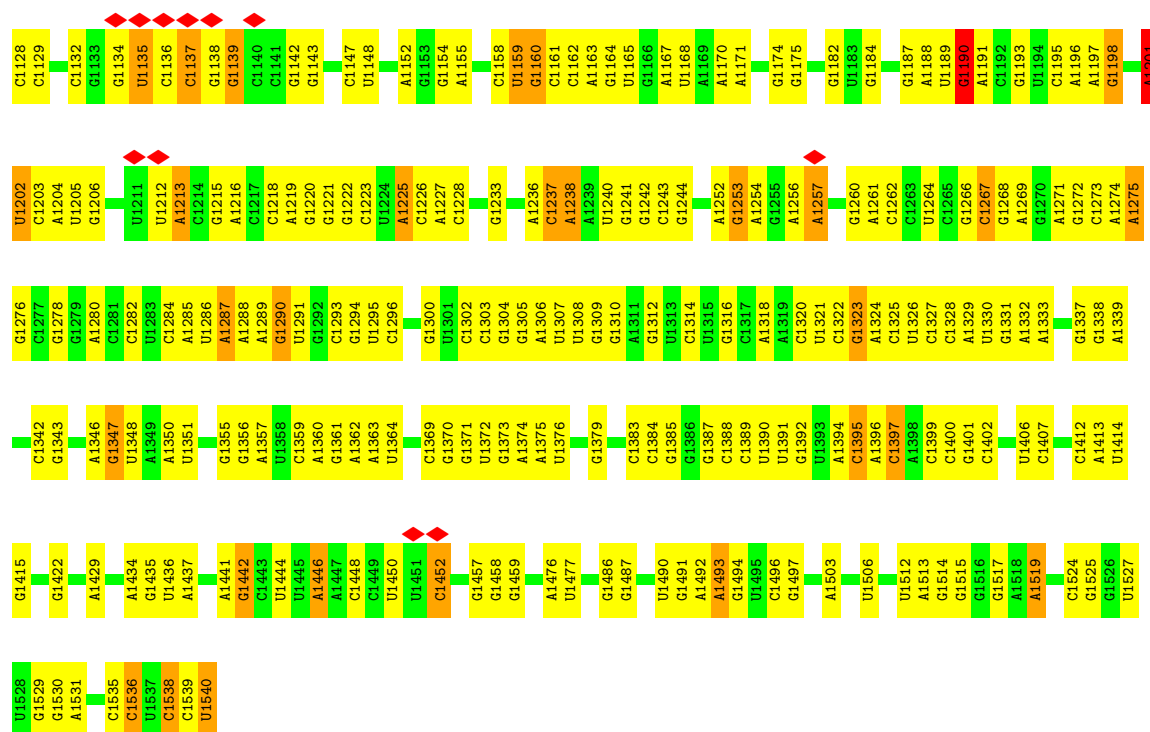
- Molecule 49: 50S ribosomal protein L1



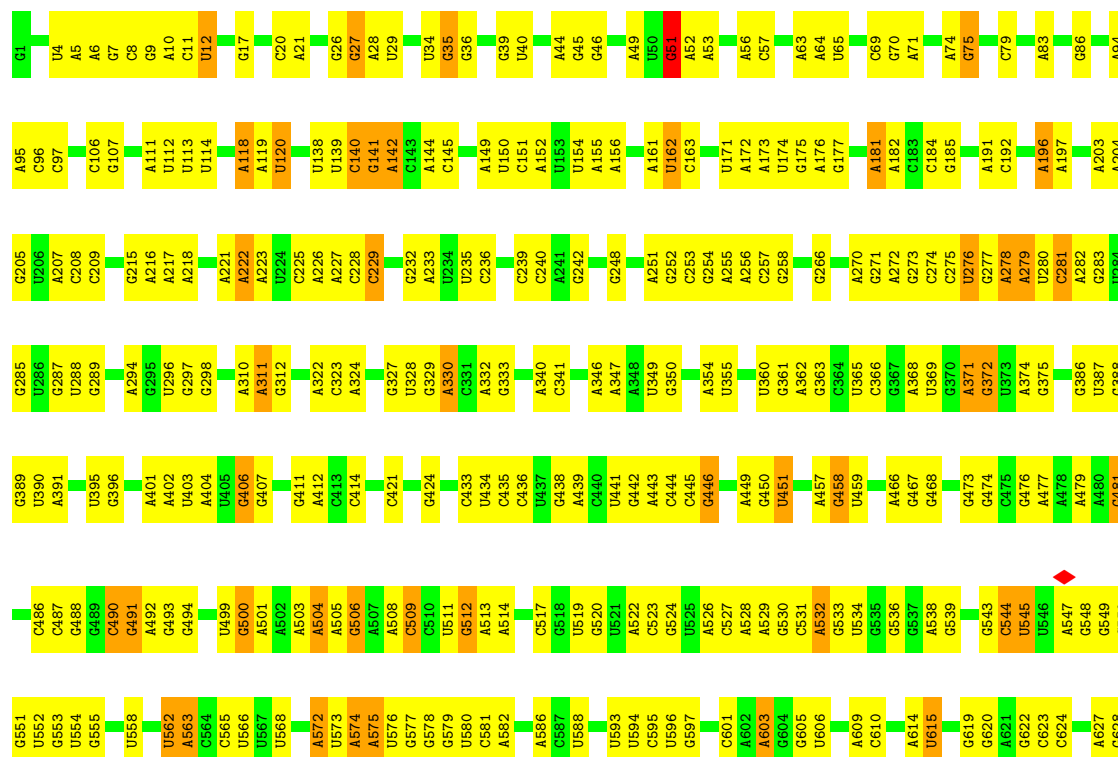
● Molecule 50: 16S ribosomal RNA

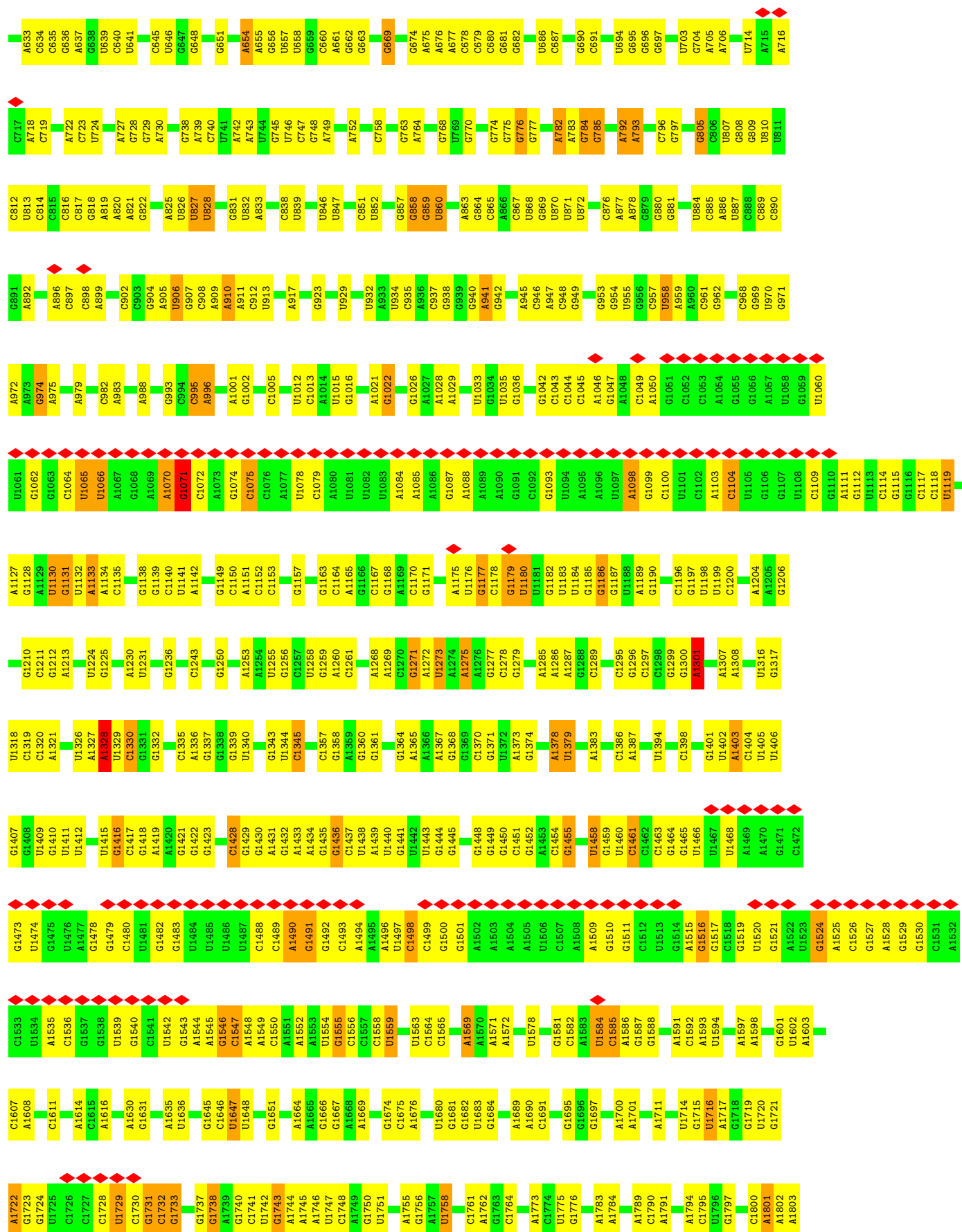
Chain 3:

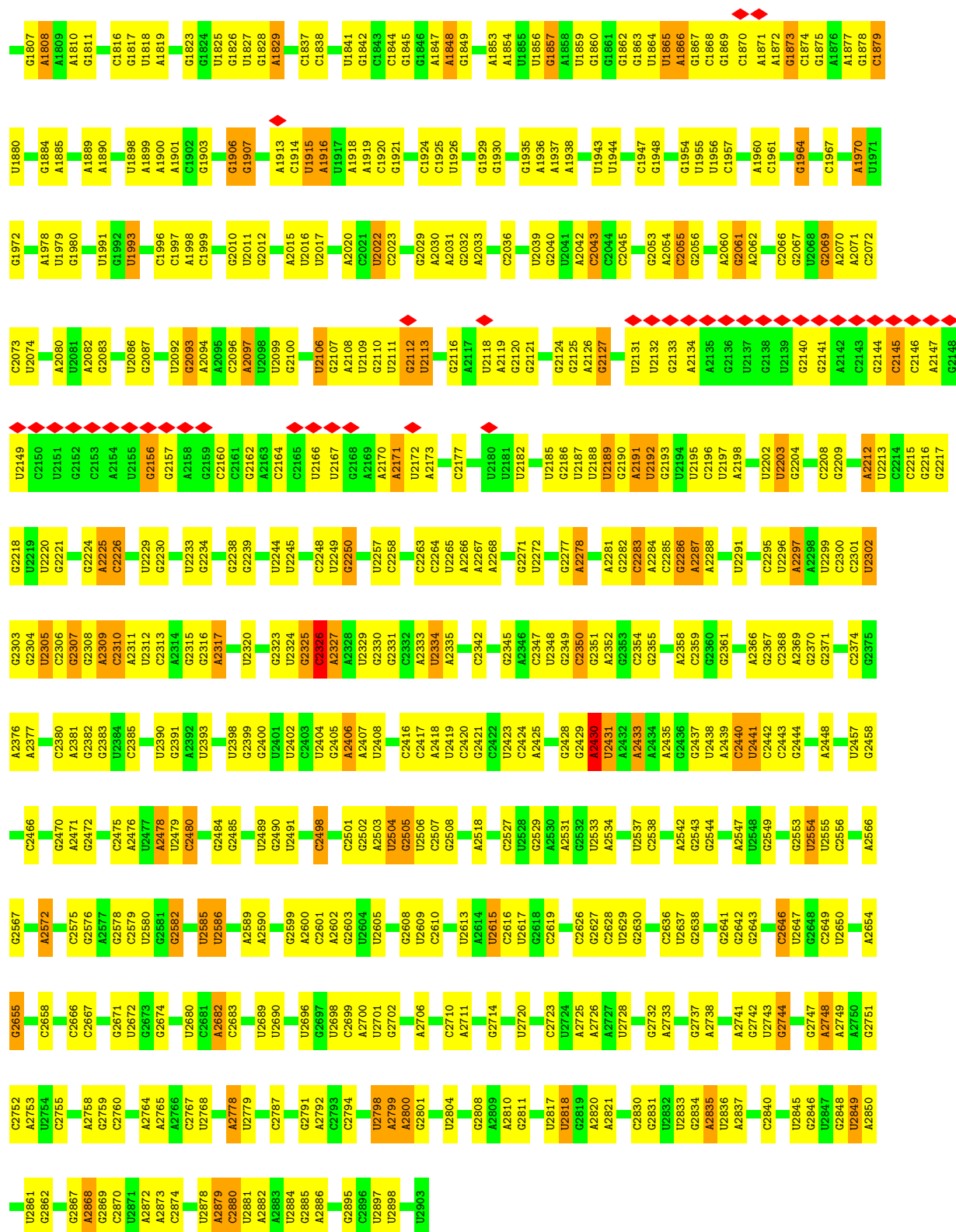


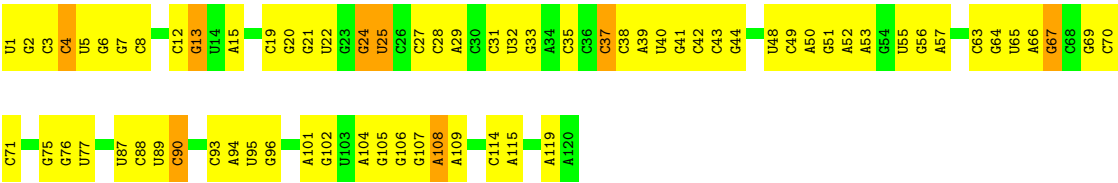


• Molecule 51: 23S ribosomal RNA

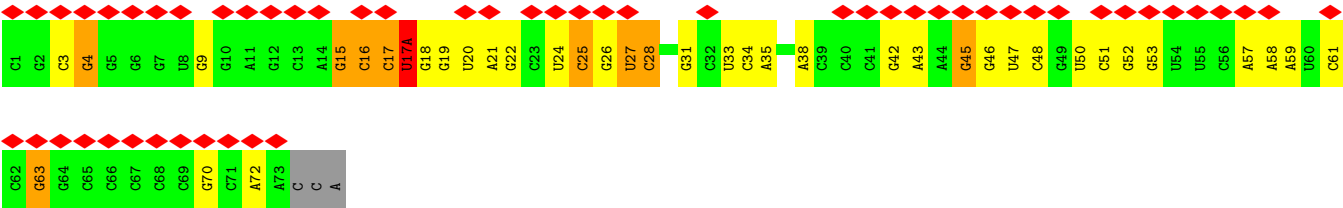




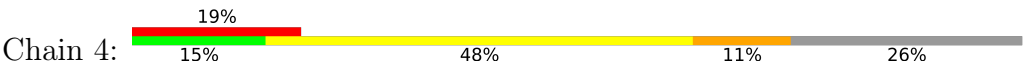




• Molecule 53: tRNAfMet



• Molecule 54: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63383	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 ($e^-/\text{\AA}^2$)	29.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	6.606	Depositor
Minimum map value	-1.704	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.400	Depositor
Recommended contour level	0.9	Depositor
Map size ($\text{\AA}$)	416.208, 416.208, 416.208	wwPDB
Map dimensions	312, 312, 312	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.334, 1.334, 1.334	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	b	0.80	9/2121 (0.4%)	1.13	24/2852 (0.8%)
2	c	0.79	3/1586 (0.2%)	1.13	12/2134 (0.6%)
3	d	0.80	6/1571 (0.4%)	1.15	12/2113 (0.6%)
4	e	1.34	22/1434 (1.5%)	1.42	32/1926 (1.7%)
5	f	1.03	9/1343 (0.7%)	1.22	19/1816 (1.0%)
6	g	1.29	14/1122 (1.2%)	1.40	24/1515 (1.6%)
7	j	0.80	2/1152 (0.2%)	1.13	10/1551 (0.6%)
8	k	0.98	5/947 (0.5%)	1.28	14/1268 (1.1%)
9	l	0.80	3/1054 (0.3%)	1.17	9/1403 (0.6%)
10	m	0.84	7/1093 (0.6%)	1.14	14/1460 (1.0%)
11	n	0.82	3/973 (0.3%)	1.17	6/1301 (0.5%)
12	o	1.01	7/902 (0.8%)	1.14	4/1209 (0.3%)
13	p	0.71	4/929 (0.4%)	1.01	2/1242 (0.2%)
14	q	0.77	3/960 (0.3%)	1.23	2/1278 (0.2%)
15	r	0.69	0/829	1.10	3/1107 (0.3%)
16	s	0.98	7/864 (0.8%)	1.20	9/1156 (0.8%)
17	t	0.99	6/744 (0.8%)	1.16	4/994 (0.4%)
18	u	0.67	2/787 (0.3%)	1.01	4/1051 (0.4%)
19	v	0.78	3/766 (0.4%)	1.00	4/1025 (0.4%)
20	w	0.58	0/582	0.96	1/769 (0.1%)
21	x	0.85	5/635 (0.8%)	1.02	2/848 (0.2%)
22	y	1.11	4/510 (0.8%)	1.37	9/677 (1.3%)
23	z	0.78	2/453 (0.4%)	0.99	1/605 (0.2%)
24	B	0.74	1/450 (0.2%)	1.00	1/599 (0.2%)
25	C	0.77	2/416 (0.5%)	0.91	3/554 (0.5%)
26	D	0.74	1/380 (0.3%)	1.19	4/498 (0.8%)
27	E	0.77	1/513 (0.2%)	1.09	1/676 (0.1%)
28	F	0.82	1/303 (0.3%)	1.19	3/397 (0.8%)
29	G	1.31	27/1787 (1.5%)	1.39	27/2408 (1.1%)
30	H	1.31	21/1651 (1.3%)	1.34	27/2225 (1.2%)
31	I	1.15	20/1665 (1.2%)	1.36	28/2227 (1.3%)
32	J	1.14	15/1169 (1.3%)	1.44	26/1573 (1.7%)
33	K	1.47	15/843 (1.8%)	1.46	24/1140 (2.1%)
34	L	1.20	14/1195 (1.2%)	1.51	35/1602 (2.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	M	0.99	5/989 (0.5%)	1.23	14/1326 (1.1%)
36	N	1.25	13/1034 (1.3%)	1.39	25/1375 (1.8%)
37	O	1.29	11/796 (1.4%)	1.39	16/1077 (1.5%)
38	P	1.71	16/885 (1.8%)	1.61	27/1195 (2.3%)
39	Q	1.28	16/969 (1.7%)	1.42	18/1300 (1.4%)
40	R	1.45	15/892 (1.7%)	1.47	23/1193 (1.9%)
41	S	1.31	11/817 (1.3%)	1.42	16/1088 (1.5%)
42	T	1.06	6/722 (0.8%)	1.38	14/964 (1.5%)
43	U	0.59	0/659	1.04	4/884 (0.5%)
44	V	0.55	1/657 (0.2%)	0.93	1/881 (0.1%)
45	W	1.15	4/544 (0.7%)	1.24	9/731 (1.2%)
46	X	2.08	22/652 (3.4%)	2.05	39/877 (4.4%)
47	Y	1.21	7/671 (1.0%)	1.28	8/888 (0.9%)
48	Z	1.12	6/550 (1.1%)	1.54	15/728 (2.1%)
49	a	1.60	21/1033 (2.0%)	1.47	28/1387 (2.0%)
50	3	0.46	2/36963 (0.0%)	0.49	11/57662 (0.0%)
51	1	0.41	0/69796	0.51	5/108888 (0.0%)
52	2	0.42	0/2872	0.51	0/4479
53	5	0.47	0/1763	0.56	1/2748 (0.0%)
54	4	0.44	0/493	0.50	0/769
All	All	0.69	400/157486 (0.3%)	0.78	674/235639 (0.3%)

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
6	g	0	1
29	G	0	1
32	J	0	1
51	1	0	18
52	2	0	2
All	All	0	23

The worst 5 of 400 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	3	967	C	C3'-O3'	26.44	1.81	1.42
50	3	968	A	O3'-P	25.76	1.99	1.61
38	P	32	THR	C-O	22.10	1.50	1.23
39	Q	78	VAL	C-O	21.33	1.49	1.24

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	P	21	HIS	C-O	19.67	1.47	1.24

The worst 5 of 674 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	X	73	PHE	CA-C-N	-16.84	102.98	122.52
46	X	73	PHE	C-N-CA	-16.84	102.98	122.52
50	3	967	C	C4'-C3'-O3'	-14.27	91.59	113.00
46	X	21	ALA	CA-C-N	-12.13	103.19	120.42
46	X	21	ALA	C-N-CA	-12.13	103.19	120.42

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
51	1	27	G	Sidechain
51	1	51	G	Sidechain
29	G	14	HIS	Mainchain
32	J	92	ARG	Mainchain
6	g	8	LYS	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2082	0	2157	88	0
2	c	1565	0	1616	49	0
3	d	1552	0	1619	48	0
4	e	1410	0	1447	106	0
5	f	1323	0	1374	42	0
6	g	1111	0	1147	69	0
7	j	1129	0	1162	47	0
8	k	938	0	1012	50	0
9	l	1045	0	1117	28	0
10	m	1074	0	1157	43	0
11	n	960	0	1000	44	0
12	o	892	0	923	48	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	p	917	0	965	43	0
14	q	947	0	1022	43	0
15	r	816	0	839	38	0
16	s	857	0	922	30	0
17	t	738	0	807	35	0
18	u	779	0	834	23	0
19	v	753	0	780	44	0
20	w	575	0	592	19	0
21	x	625	0	655	20	0
22	y	509	0	543	25	0
23	z	449	0	491	27	0
24	B	444	0	461	28	0
25	C	409	0	440	16	0
26	D	377	0	418	14	0
27	E	504	0	574	14	0
28	F	302	0	343	16	0
29	G	1756	0	1787	95	0
30	H	1624	0	1699	117	0
31	I	1643	0	1710	123	0
32	J	1156	0	1199	49	0
33	K	824	0	815	60	0
34	L	1181	0	1240	66	0
35	M	979	0	1034	49	0
36	N	1022	0	1070	66	0
37	O	786	0	828	61	0
38	P	869	0	878	68	0
39	Q	955	0	1019	62	0
40	R	883	0	944	81	0
41	S	805	0	847	55	0
42	T	714	0	737	47	0
43	U	649	0	666	40	0
44	V	648	0	691	34	0
45	W	535	0	552	36	0
46	X	637	0	665	61	0
47	Y	665	0	714	29	0
48	Z	544	0	579	37	0
49	a	1026	0	1092	60	0
50	3	33012	0	16618	709	0
51	1	62317	0	31346	1065	0
52	2	2568	0	1303	72	0
53	5	1578	0	804	27	0
54	4	437	0	219	15	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	144895	0	97473	3806	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 16.

The worst 5 of 3806 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)
50:3:967:C:C3'	50:3:967:C:O3'	1.81	1.25
50:3:968:A:O3'	50:3:969:A:P	1.99	1.20
51:1:783:A:H2'	51:1:784:G:H4'	1.22	1.14
50:3:405:U:H3'	50:3:406:G:H5'	1.31	1.08
52:2:3:C:H3'	52:2:4:C:H5''	1.36	1.08

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	b	269/273 (98%)	244 (91%)	24 (9%)	1 (0%)	30	59
2	c	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
3	d	199/201 (99%)	184 (92%)	14 (7%)	1 (0%)	24	54
4	e	175/179 (98%)	150 (86%)	24 (14%)	1 (1%)	21	50
5	f	174/177 (98%)	154 (88%)	18 (10%)	2 (1%)	11	38
6	g	147/149 (99%)	118 (80%)	25 (17%)	4 (3%)	4	20
7	j	140/142 (99%)	132 (94%)	7 (5%)	1 (1%)	18	47
8	k	120/123 (98%)	110 (92%)	9 (8%)	1 (1%)	16	44
9	l	141/144 (98%)	128 (91%)	13 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	m	134/136 (98%)	117 (87%)	14 (10%)	3 (2%)	5	24
11	n	118/127 (93%)	102 (86%)	16 (14%)	0	100	100
12	o	114/117 (97%)	106 (93%)	8 (7%)	0	100	100
13	p	112/115 (97%)	97 (87%)	15 (13%)	0	100	100
14	q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
15	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
16	s	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
17	t	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
18	u	100/104 (96%)	87 (87%)	12 (12%)	1 (1%)	12	40
19	v	92/94 (98%)	87 (95%)	4 (4%)	1 (1%)	11	38
20	w	73/85 (86%)	68 (93%)	5 (7%)	0	100	100
21	x	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
22	y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
23	z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
24	B	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
25	C	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
26	D	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
27	E	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	7	29
28	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	19
29	G	223/241 (92%)	193 (86%)	28 (13%)	2 (1%)	14	42
30	H	204/233 (88%)	187 (92%)	17 (8%)	0	100	100
31	I	203/206 (98%)	184 (91%)	19 (9%)	0	100	100
32	J	155/167 (93%)	128 (83%)	23 (15%)	4 (3%)	4	21
33	K	99/131 (76%)	81 (82%)	14 (14%)	4 (4%)	2	15
34	L	149/156 (96%)	135 (91%)	14 (9%)	0	100	100
35	M	127/130 (98%)	118 (93%)	8 (6%)	1 (1%)	16	44
36	N	125/130 (96%)	99 (79%)	23 (18%)	3 (2%)	4	22
37	O	96/103 (93%)	79 (82%)	16 (17%)	1 (1%)	12	40
38	P	114/129 (88%)	93 (82%)	20 (18%)	1 (1%)	14	42
39	Q	121/124 (98%)	95 (78%)	24 (20%)	2 (2%)	7	28
40	R	112/118 (95%)	101 (90%)	10 (9%)	1 (1%)	14	42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	S	98/101 (97%)	84 (86%)	13 (13%)	1 (1%)	12	40
42	T	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	10	35
43	U	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
44	V	78/84 (93%)	67 (86%)	11 (14%)	0	100	100
45	W	63/75 (84%)	58 (92%)	5 (8%)	0	100	100
46	X	77/92 (84%)	68 (88%)	9 (12%)	0	100	100
47	Y	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
48	Z	63/71 (89%)	37 (59%)	23 (36%)	3 (5%)	2	11
49	a	130/234 (56%)	120 (92%)	10 (8%)	0	100	100
All	All	5652/6050 (93%)	5030 (89%)	580 (10%)	42 (1%)	20	47

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
6	g	9	VAL
6	g	11	ASN
18	u	18	LYS
27	E	31	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/218 (99%)	216 (100%)	0	100	100
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	72
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	80
4	e	148/150 (99%)	145 (98%)	3 (2%)	48	65
5	f	137/138 (99%)	136 (99%)	1 (1%)	76	78
6	g	114/114 (100%)	114 (100%)	0	100	100
7	j	116/116 (100%)	116 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	k	103/104 (99%)	103 (100%)	0	100	100
9	l	102/103 (99%)	102 (100%)	0	100	100
10	m	109/109 (100%)	109 (100%)	0	100	100
11	n	100/104 (96%)	100 (100%)	0	100	100
12	o	86/87 (99%)	85 (99%)	1 (1%)	63	72
13	p	99/100 (99%)	99 (100%)	0	100	100
14	q	89/90 (99%)	89 (100%)	0	100	100
15	r	84/84 (100%)	84 (100%)	0	100	100
16	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
17	t	80/84 (95%)	80 (100%)	0	100	100
18	u	83/85 (98%)	83 (100%)	0	100	100
19	v	78/78 (100%)	78 (100%)	0	100	100
20	w	57/63 (90%)	57 (100%)	0	100	100
21	x	67/68 (98%)	67 (100%)	0	100	100
22	y	55/55 (100%)	55 (100%)	0	100	100
23	z	48/49 (98%)	48 (100%)	0	100	100
24	B	47/48 (98%)	47 (100%)	0	100	100
25	C	45/49 (92%)	45 (100%)	0	100	100
26	D	38/38 (100%)	38 (100%)	0	100	100
27	E	51/52 (98%)	51 (100%)	0	100	100
28	F	34/34 (100%)	34 (100%)	0	100	100
29	G	186/199 (94%)	185 (100%)	1 (0%)	81	81
30	H	170/190 (90%)	170 (100%)	0	100	100
31	I	172/173 (99%)	171 (99%)	1 (1%)	78	80
32	J	119/126 (94%)	119 (100%)	0	100	100
33	K	88/112 (79%)	87 (99%)	1 (1%)	65	74
34	L	124/129 (96%)	124 (100%)	0	100	100
35	M	104/105 (99%)	103 (99%)	1 (1%)	68	75
36	N	105/107 (98%)	103 (98%)	2 (2%)	50	66
37	O	86/90 (96%)	85 (99%)	1 (1%)	63	72
38	P	89/99 (90%)	89 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Q	103/104 (99%)	103 (100%)	0	100	100
40	R	92/96 (96%)	92 (100%)	0	100	100
41	S	83/84 (99%)	82 (99%)	1 (1%)	63	72
42	T	76/77 (99%)	76 (100%)	0	100	100
43	U	65/65 (100%)	63 (97%)	2 (3%)	35	59
44	V	74/78 (95%)	73 (99%)	1 (1%)	59	70
45	W	56/65 (86%)	56 (100%)	0	100	100
46	X	70/79 (89%)	69 (99%)	1 (1%)	59	70
47	Y	65/66 (98%)	65 (100%)	0	100	100
48	Z	55/61 (90%)	54 (98%)	1 (2%)	51	67
49	a	110/181 (61%)	109 (99%)	1 (1%)	70	76
All	All	4700/4928 (95%)	4677 (100%)	23 (0%)	78	81

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	N	65	THR
43	U	47	GLU
41	S	32	ASP
43	U	74	LEU
5	f	129	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 129 such sidechains are listed below:

Mol	Chain	Res	Type
43	U	26	ASN
46	X	55	GLN
13	p	11	GLN
13	p	9	GLN
47	Y	20	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	1538/1539 (99%)	189 (12%)	2 (0%)
51	1	2902/2903 (99%)	422 (14%)	8 (0%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	2	119/120 (99%)	16 (13%)	0
53	5	73/77 (94%)	22 (30%)	1 (1%)
54	4	19/27 (70%)	7 (36%)	0
All	All	4651/4666 (99%)	656 (14%)	11 (0%)

5 of 656 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	3	A
50	3	5	U
50	3	6	G
50	3	9	G
50	3	22	G

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	2286	G
51	1	2326	C
53	5	17(A)	U
51	1	2430	A
51	1	858	G

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
50	3	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	3	968:A	O3'	969:A	P	1.99

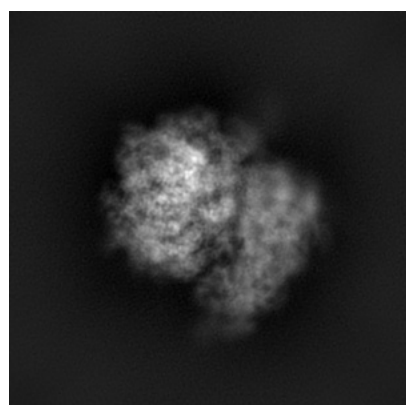
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20058. These allow visual inspection of the internal detail of the map and identification of artifacts.

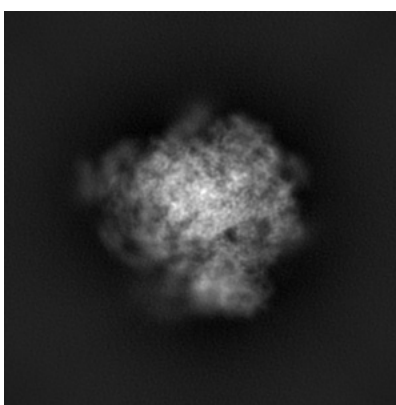
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

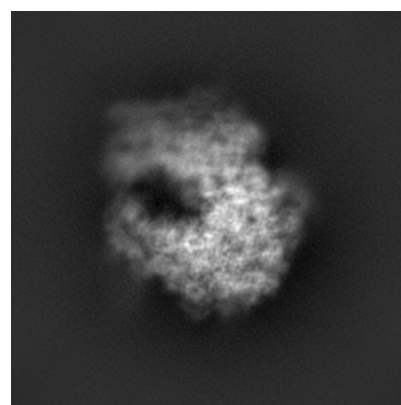
6.1.1 Primary map



X



Y

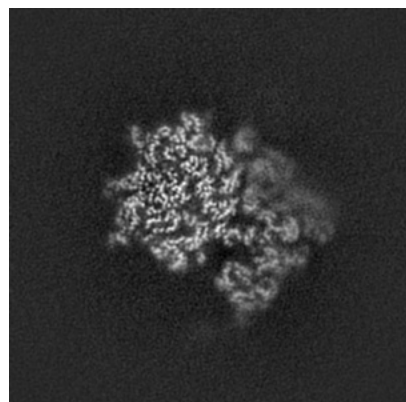


Z

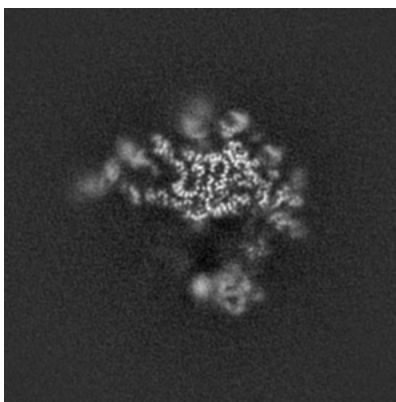
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

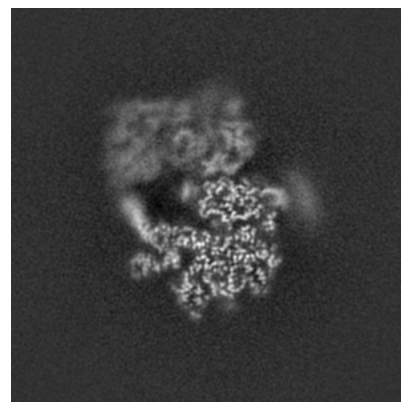
6.2.1 Primary map



X Index: 156



Y Index: 156

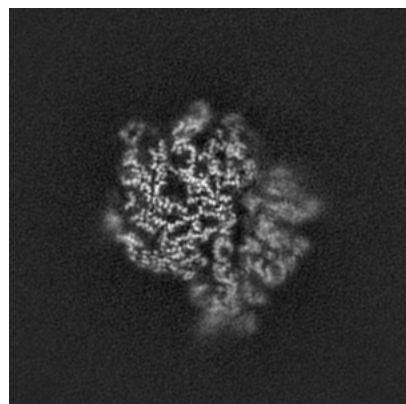


Z Index: 156

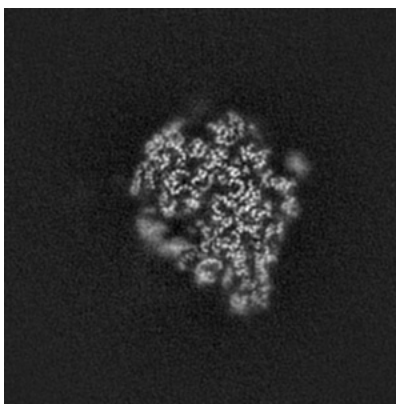
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

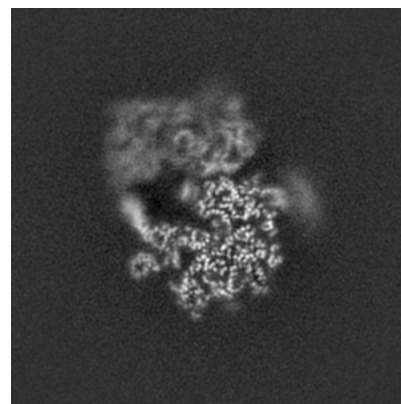
6.3.1 Primary map



X Index: 176



Y Index: 139

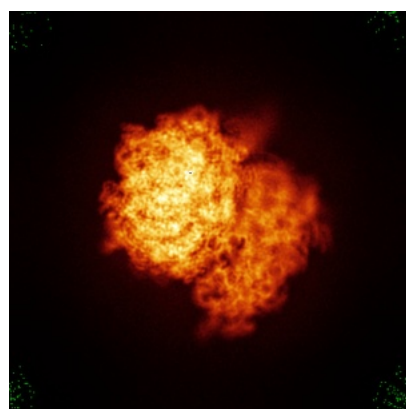


Z Index: 155

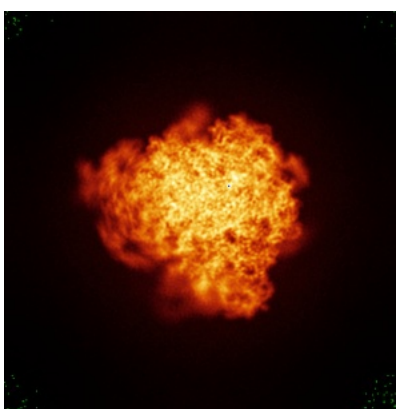
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

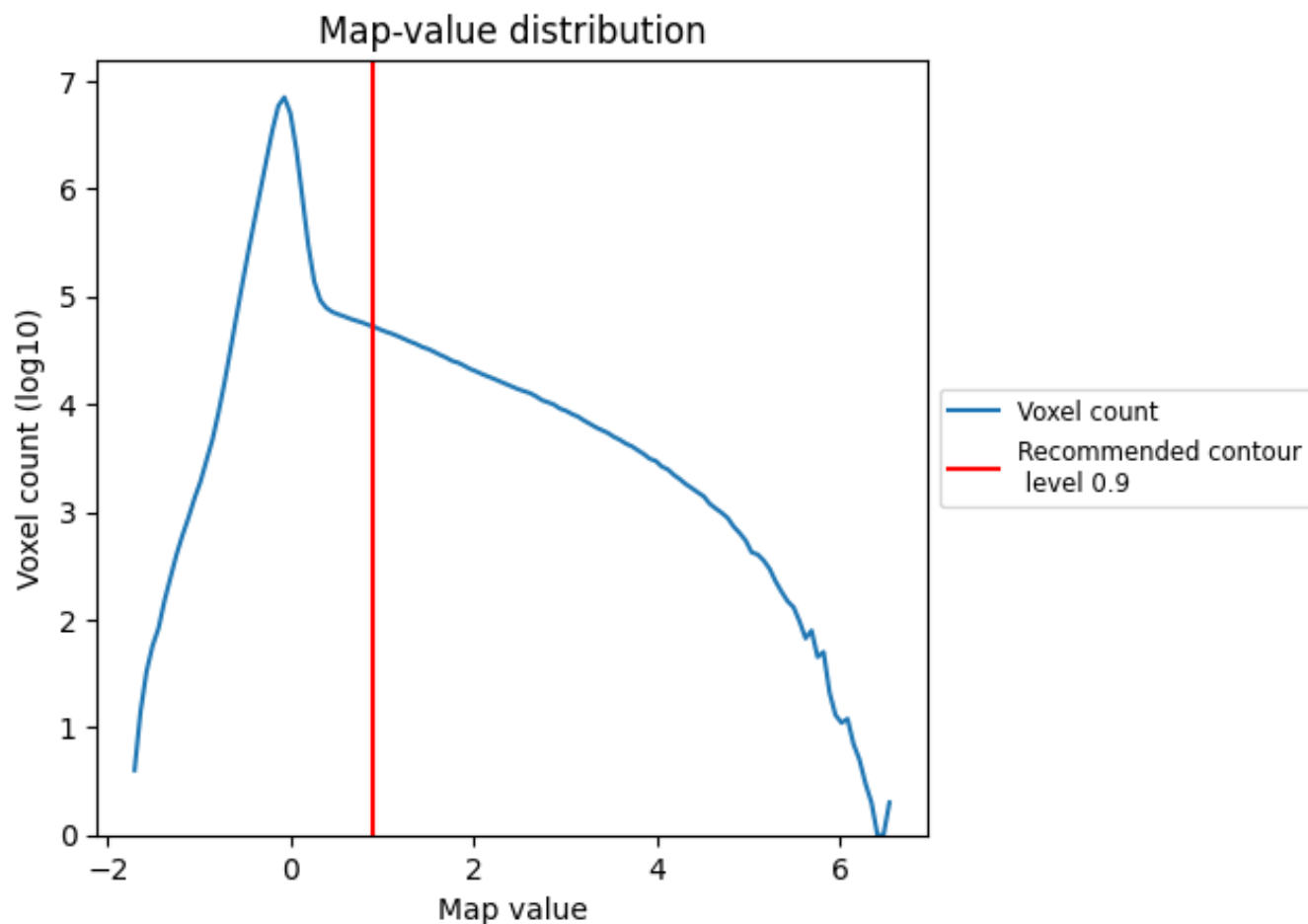
6.6 Mask visualisation

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

7 Map analysis [i](#)

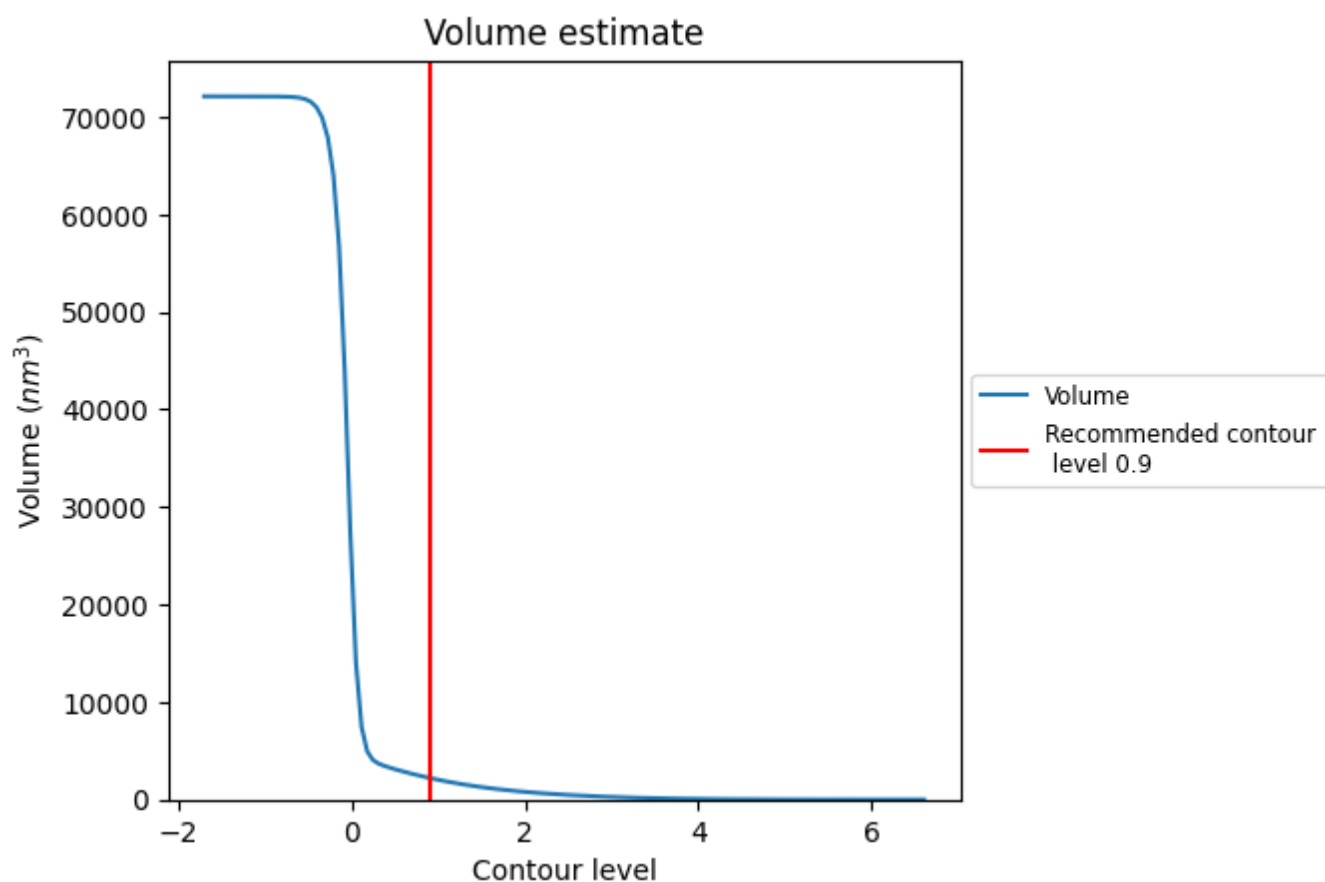
This section contains the results of statistical analysis of the map.

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.

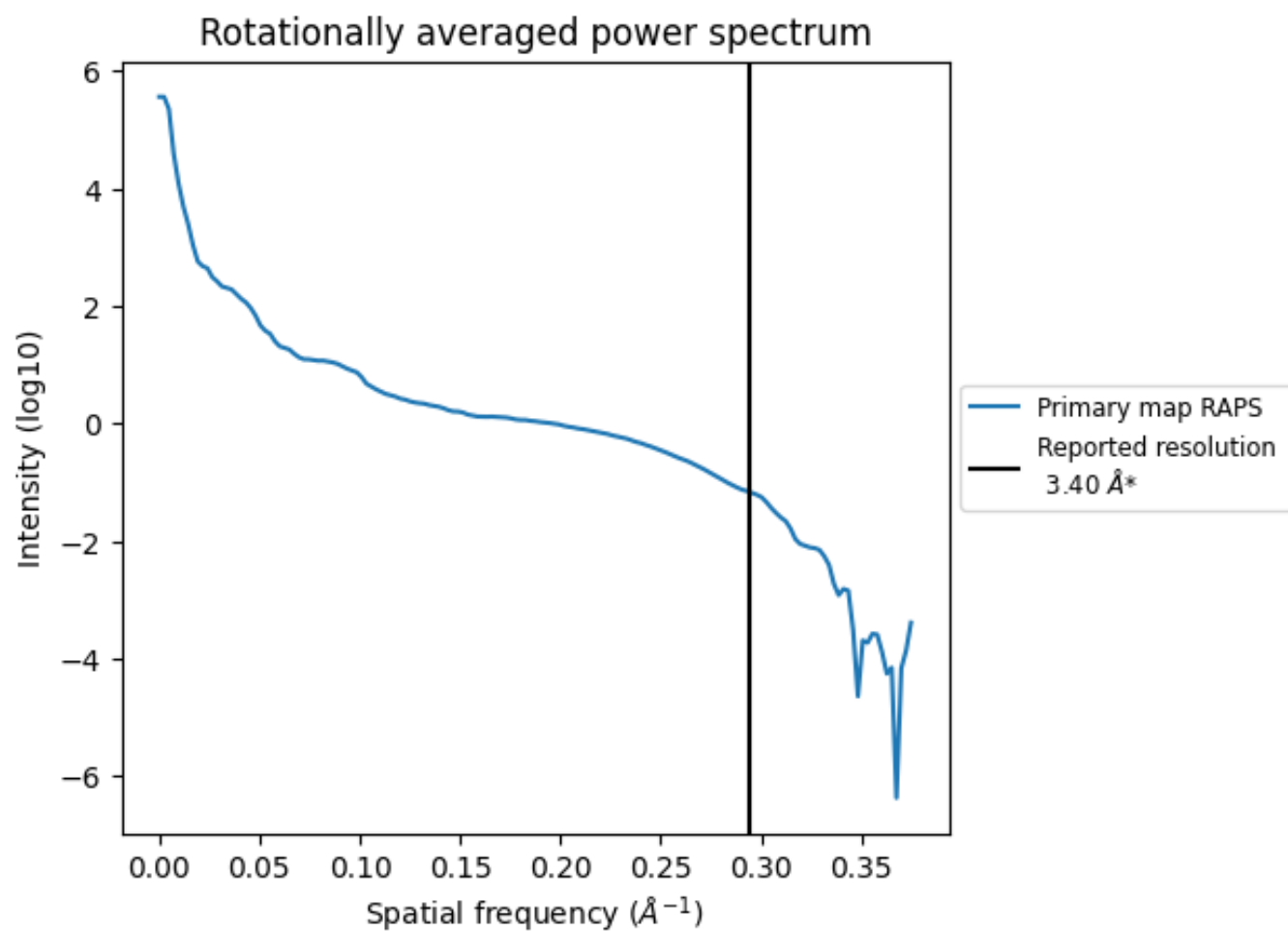
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2210 nm³; this corresponds to an approximate mass of 1996 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 0.294 Å⁻¹

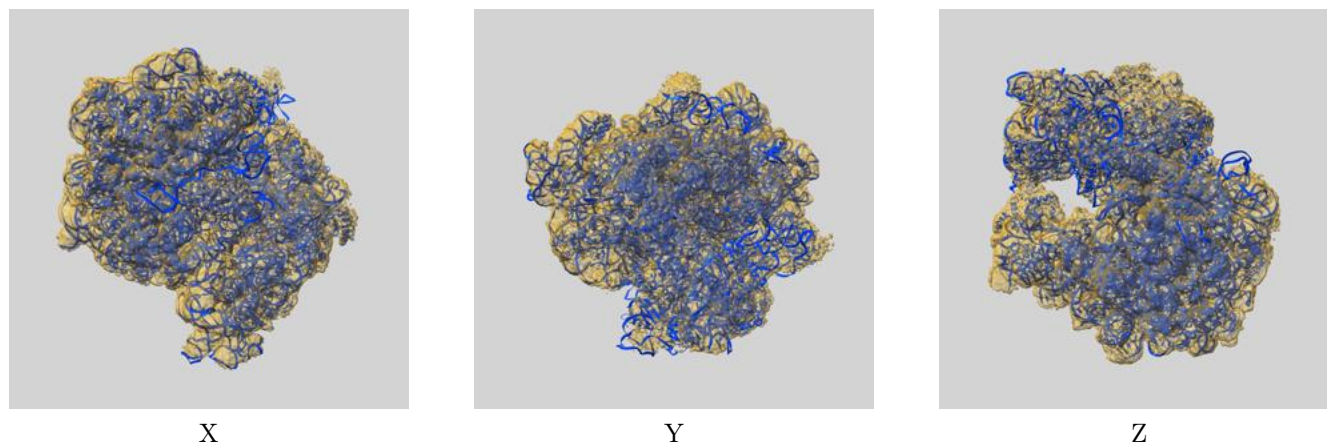
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

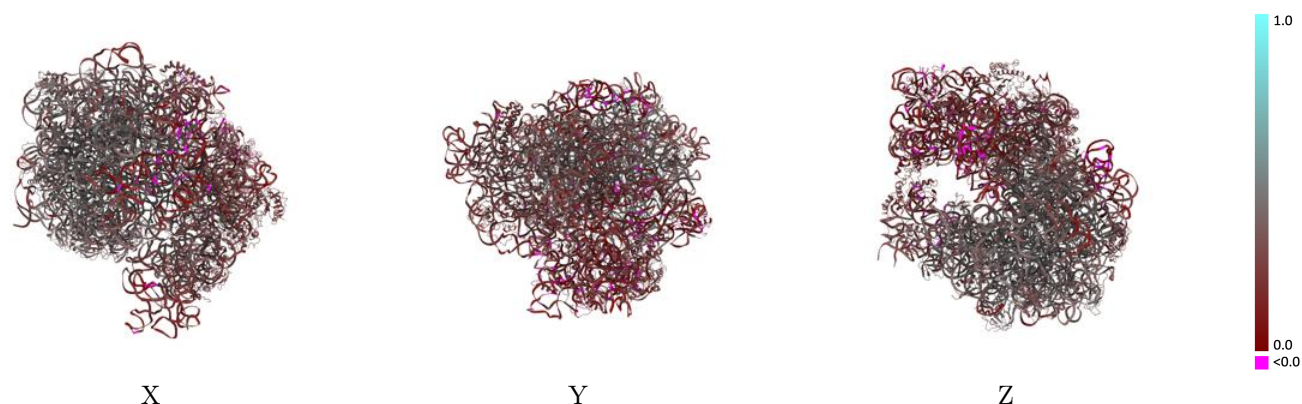
This section contains information regarding the fit between EMDB map EMD-20058 and PDB model 6OGI. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

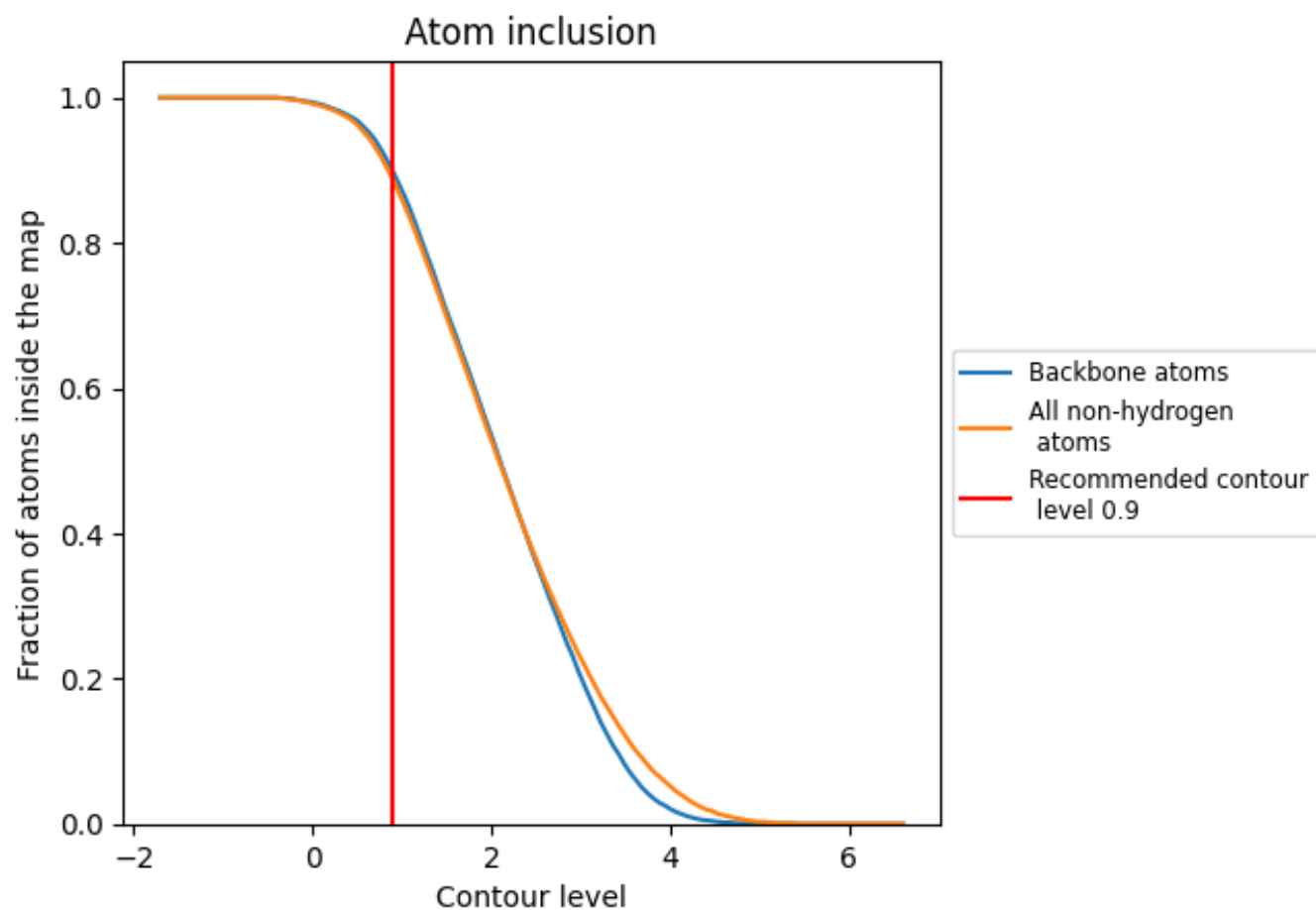


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 89% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8870	 0.3210
1	 0.9260	 0.3610
2	 0.9890	 0.3200
3	 0.9310	 0.2560
4	 0.7090	 0.1790
5	 0.2810	 0.0870
B	 0.9460	 0.4210
C	 0.9130	 0.3840
D	 0.9380	 0.4220
E	 0.9410	 0.4210
F	 0.9800	 0.3400
G	 0.6230	 0.2520
H	 0.4820	 0.2280
I	 0.7680	 0.2470
J	 0.9030	 0.2940
K	 0.8620	 0.2430
L	 0.4440	 0.2240
M	 0.9150	 0.2840
N	 0.6840	 0.1970
O	 0.4010	 0.2210
P	 0.8010	 0.2200
Q	 0.8520	 0.3090
R	 0.6130	 0.1960
S	 0.7660	 0.2030
T	 0.8880	 0.2510
U	 0.8990	 0.3420
V	 0.9430	 0.3250
W	 0.9420	 0.2780
X	 0.7250	 0.1720
Y	 0.8710	 0.2600
Z	 0.6020	 0.2070
a	 0.3000	 0.1960
b	 0.9440	 0.4120
c	 0.9650	 0.4340
d	 0.9260	 0.3970



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
e	 0.9070	 0.2310
f	 0.7140	 0.2940
g	 0.3640	 0.3010
j	 0.9440	 0.4160
k	 0.9450	 0.4250
l	 0.9460	 0.4170
m	 0.9530	 0.4110
n	 0.9570	 0.4260
o	 0.9540	 0.3270
p	 0.9370	 0.4030
q	 0.9550	 0.4160
r	 0.9330	 0.4150
s	 0.9320	 0.4260
t	 0.9350	 0.4000
u	 0.9520	 0.3920
v	 0.9540	 0.3610
w	 0.9500	 0.4320
x	 0.9330	 0.3970
y	 0.9030	 0.3250
z	 0.9340	 0.4070