



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:05 AM UTC

PDB ID : 3JCD / pdb_00003jcd
EMDB ID : EMD-6549
Title : Structure of Escherichia coli EF4 in posttranslocational ribosomes (Post EF4)
Authors : Zhang, D.; Yan, K.; Liu, G.; Song, G.; Luo, J.; Shi, Y.; Cheng, E.; Wu, S.;
Jiang, T.; Low, J.; Gao, N.; Qin, Y.
Deposited on : 2015-12-01
Resolution : 3.70 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:

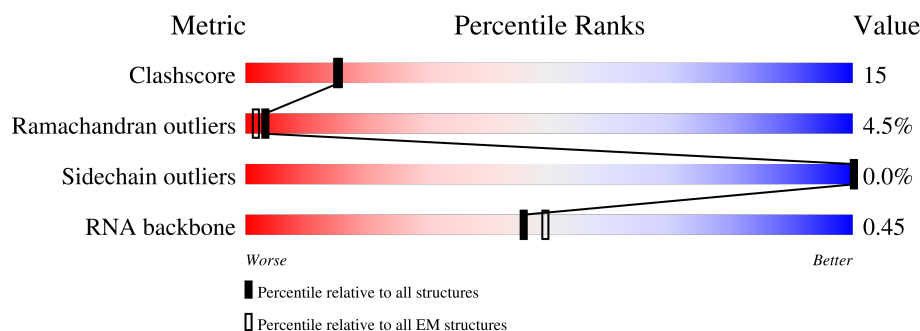
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	241	45% 55% 32% 10%
2	c	233	42% 62% 27% 12%
3	d	206	46% 55% 42% .
4	e	167	50% 59% 29% 10%
5	f	135	23% 52% 20% 24%
6	g	179	40% 50% 32% 16%
7	h	130	39% 59% 38% ..

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Mol	Chain	Length	Quality of chain
8	i	130	
9	j	103	
10	k	129	
11	l	124	
12	m	118	
13	n	101	
14	o	89	
15	p	82	
16	q	84	
17	r	75	
18	s	92	
19	t	87	
20	u	71	
21	0	57	
22	1	55	
23	2	46	
24	3	64	
25	4	38	
26	5	234	
27	C	273	
28	D	209	
29	E	201	
30	F	179	
31	G	177	
32	H	149	

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Mol	Chain	Length	Quality of chain
33	I	142	
34	J	142	
35	K	123	
36	L	144	
37	M	136	
38	N	127	
39	O	117	
40	P	115	
41	Q	118	
42	R	103	
43	S	110	
44	T	100	
45	U	104	
46	V	94	
47	W	85	
48	X	78	
49	Y	63	
50	Z	59	
51	x	599	
52	a	1533	
53	A	2904	
54	B	120	
55	7	15	
56	8	76	
56	9	76	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 147815 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 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 2 is a protein called 30S ribosomal protein S3.

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

- Molecule 3 is a protein called 30S ribosomal protein S4.

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

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	102	Total	C	N	O	S	0	0
			832	525	150	150	7		

- Molecule 6 is a protein called 30S ribosomal protein S7.

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

- Molecule 7 is a protein called 30S ribosomal protein S8.

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

- Molecule 8 is a protein called 30S ribosomal protein S9.

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

- Molecule 9 is a protein called 30S ribosomal protein S10.

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

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 11 is a protein called 30S ribosomal protein S12.

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

- Molecule 12 is a protein called 30S ribosomal protein S13.

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

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

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

- Molecule 15 is a protein called 30S ribosomal protein S16.

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

- Molecule 16 is a protein called 30S ribosomal protein S17.

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

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	r	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 18 is a protein called 30S ribosomal protein S19.

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

- Molecule 19 is a protein called 30S ribosomal protein S20.

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

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	u	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 22 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 24 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 25 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 26 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	5	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	270	Total	C	N	O	S	0	0
			2076	1285	422	362	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 51 is a protein called Elongation factor 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	26	Total	C	N	O	S	0	0
			214	134	43	35	2		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	2903	Total	C	N	O	P	0	0
			62320	27801	11467	20149	2903		

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

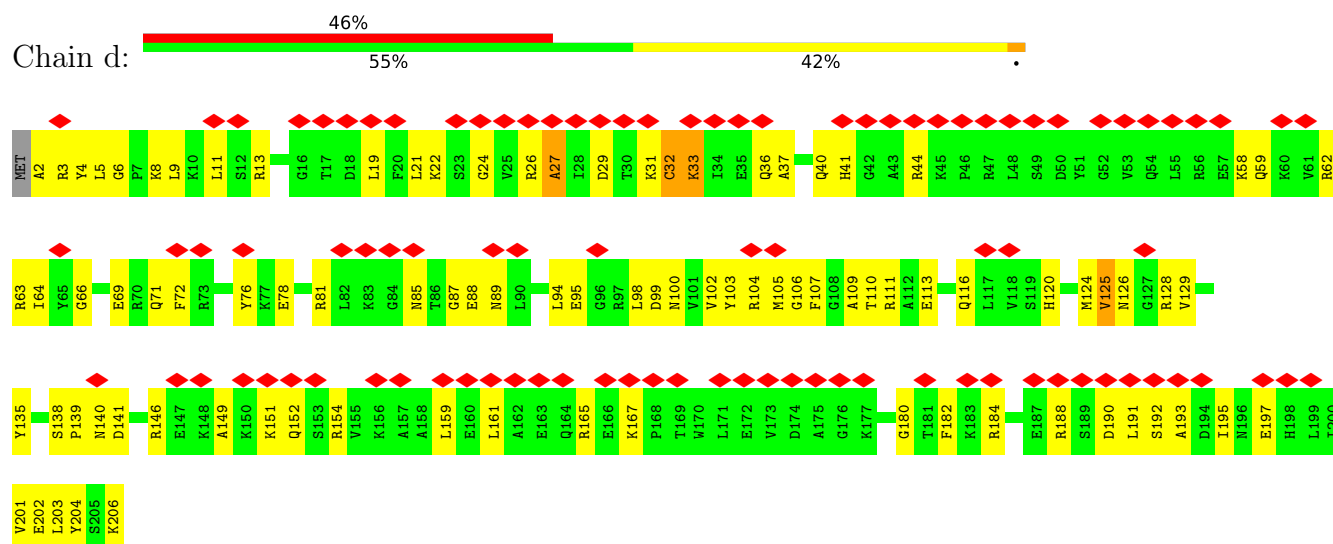
Mol	Chain	Residues	Atoms					AltConf	Trace
54	B	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 55 is a RNA chain called mRNA.

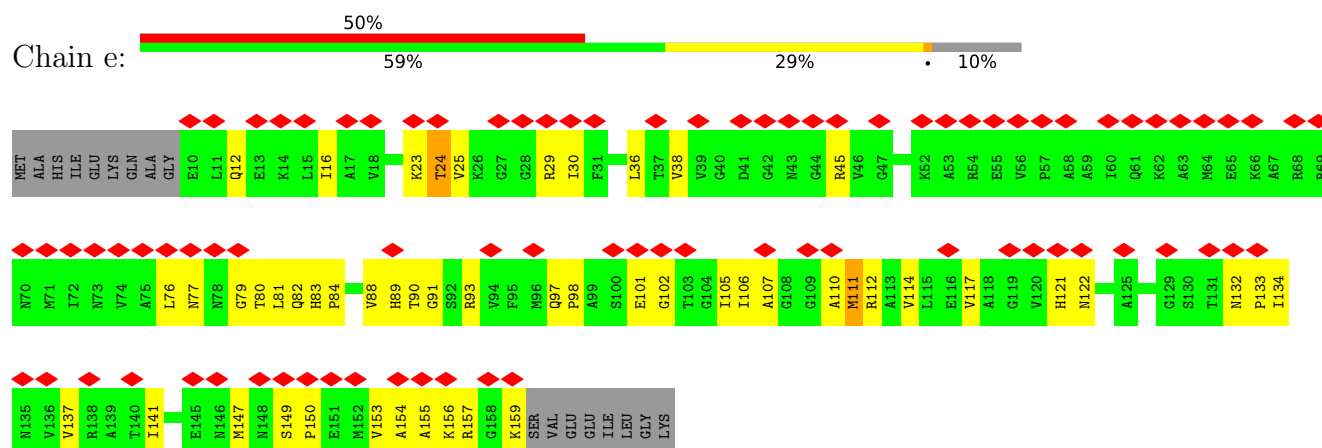
Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	9	Total	C	N	O	P	0	0
			191	86	34	62	9		

- Molecule 56 is a RNA chain called tRNA.

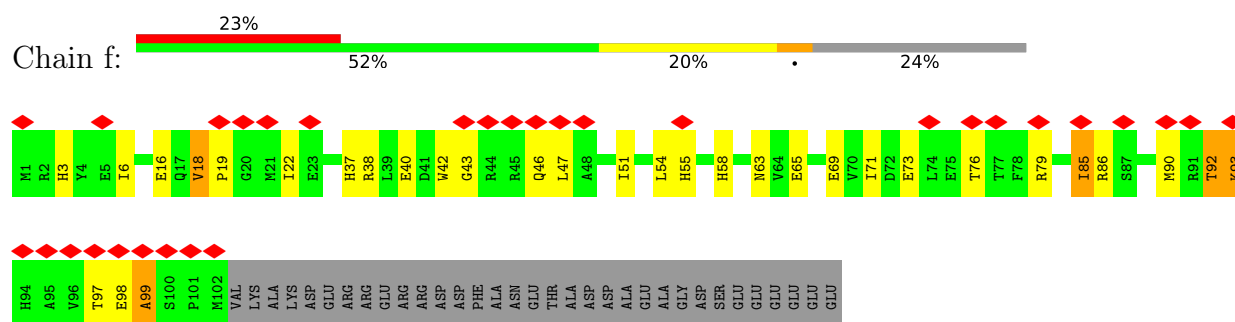
Mol	Chain	Residues	Atoms					AltConf	Trace
56	8	76	Total 1623	C 723	N 290	O 534	P 76	0	0
56	9	76	Total 1623	C 723	N 290	O 534	P 76	0	0



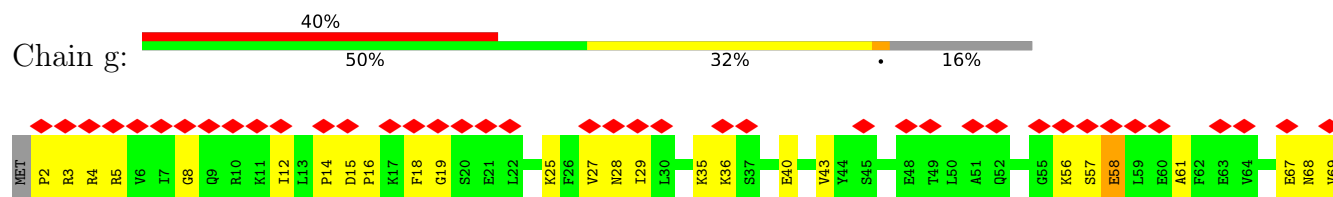
• Molecule 4: 30S ribosomal protein S5

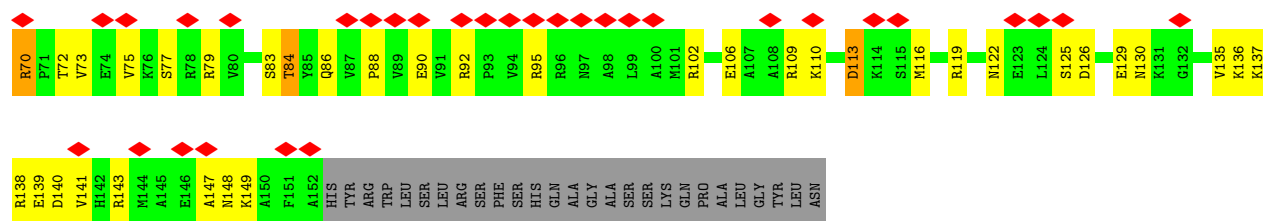


• Molecule 5: 30S ribosomal protein S6

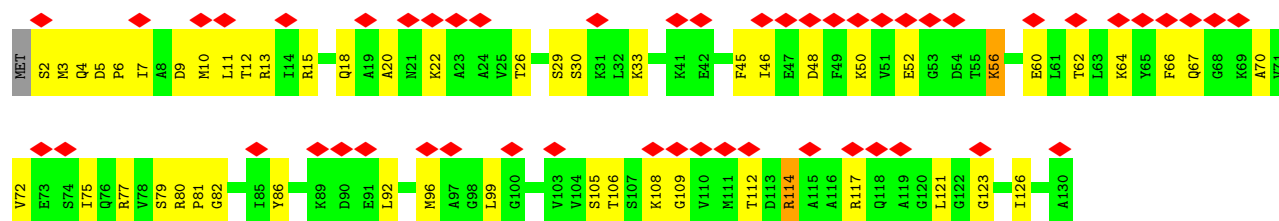
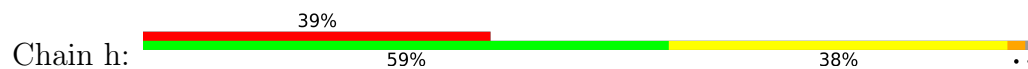


• Molecule 6: 30S ribosomal protein S7

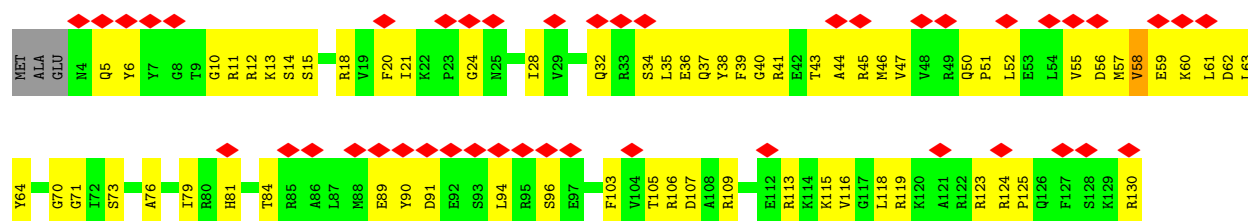




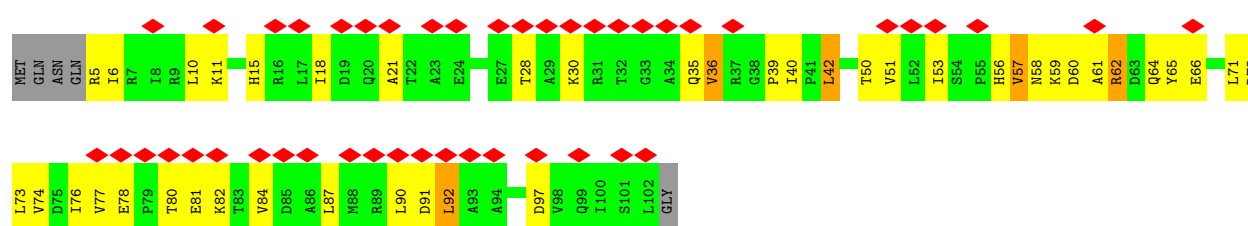
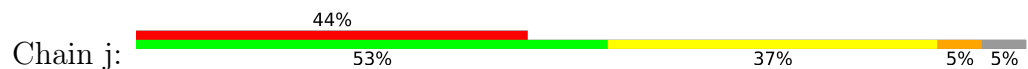
• Molecule 7: 30S ribosomal protein S8



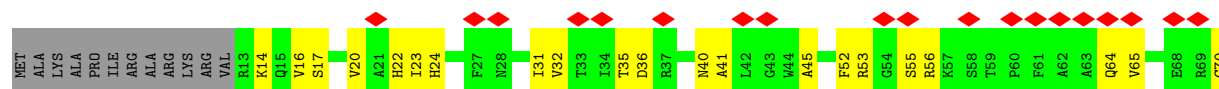
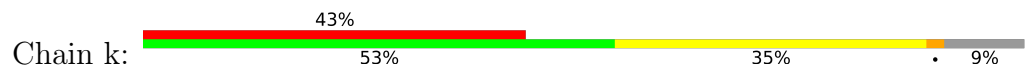
• Molecule 8: 30S ribosomal protein S9



• Molecule 9: 30S ribosomal protein S10

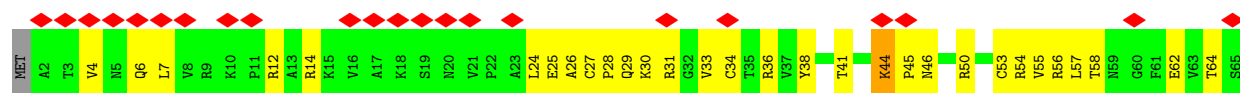


• Molecule 10: 30S ribosomal protein S11





- Molecule 11: 30S ribosomal protein S12



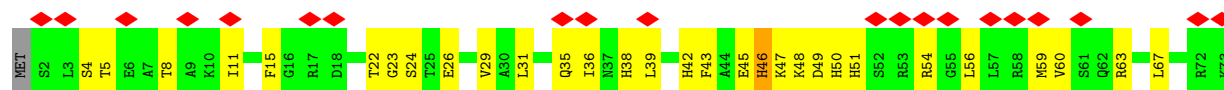
- Molecule 12: 30S ribosomal protein S13



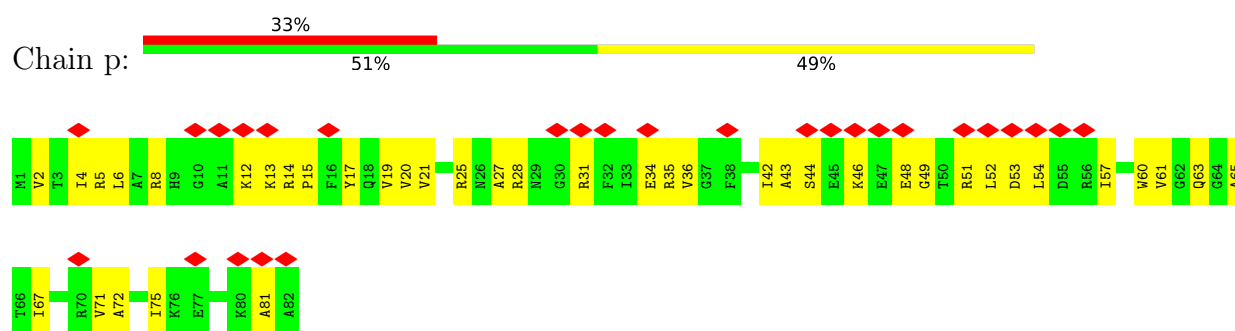
- Molecule 13: 30S ribosomal protein S14



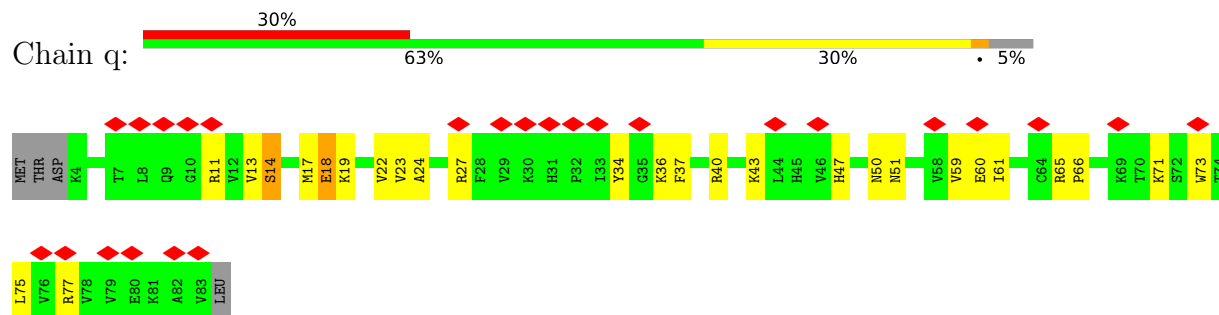
- Molecule 14: 30S ribosomal protein S15



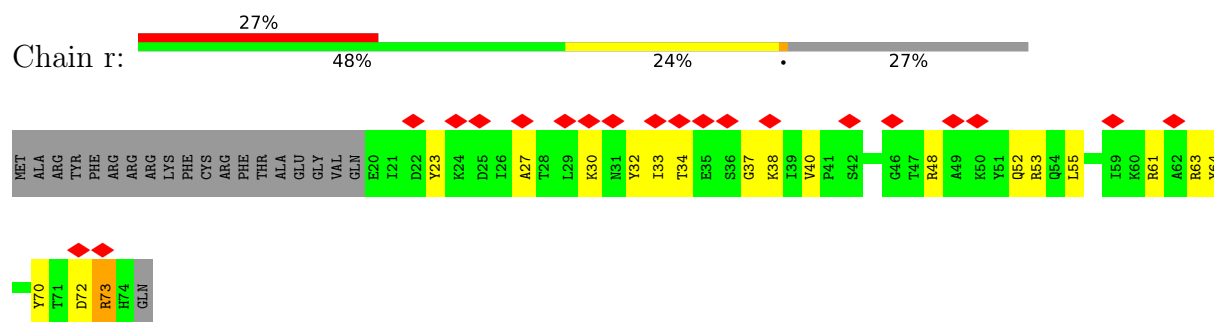
- Molecule 15: 30S ribosomal protein S16



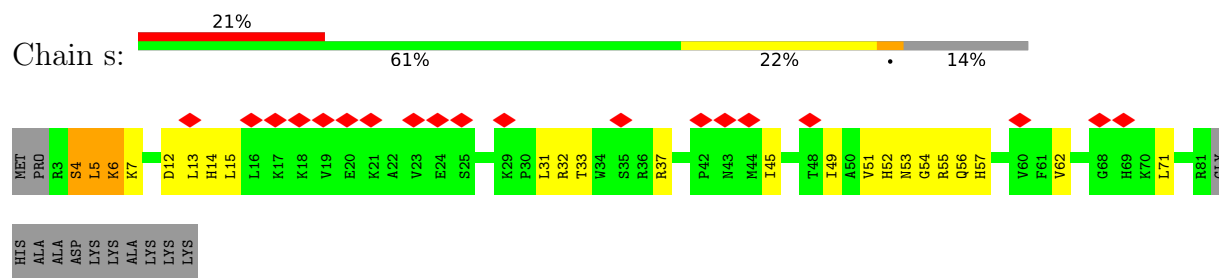
- Molecule 16: 30S ribosomal protein S17



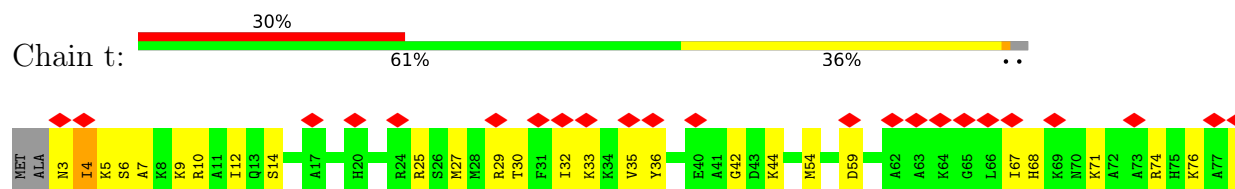
- Molecule 17: 30S ribosomal protein S18

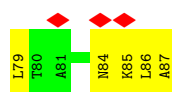


- Molecule 18: 30S ribosomal protein S19

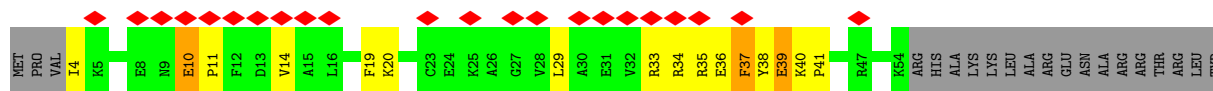


- Molecule 19: 30S ribosomal protein S20

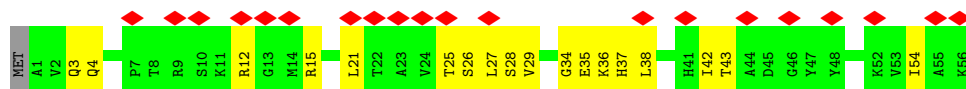




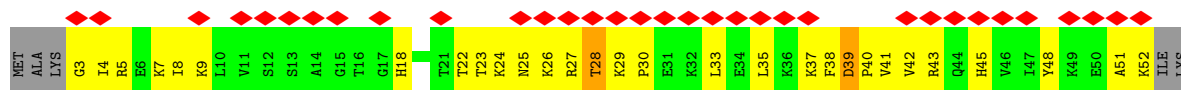
- Molecule 20: 30S ribosomal protein S21



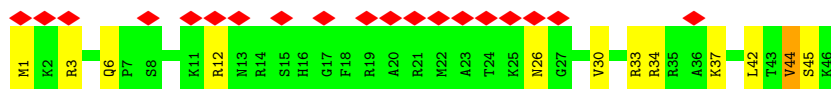
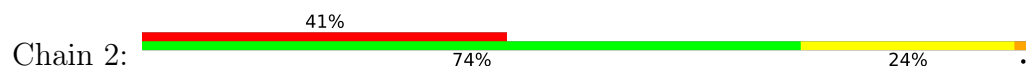
- Molecule 21: 50S ribosomal protein L32



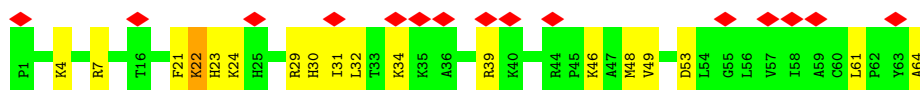
- Molecule 22: 50S ribosomal protein L33



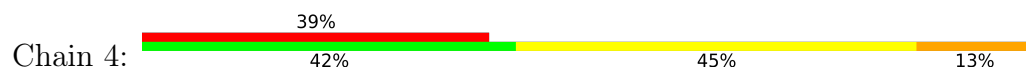
- Molecule 23: 50S ribosomal protein L34



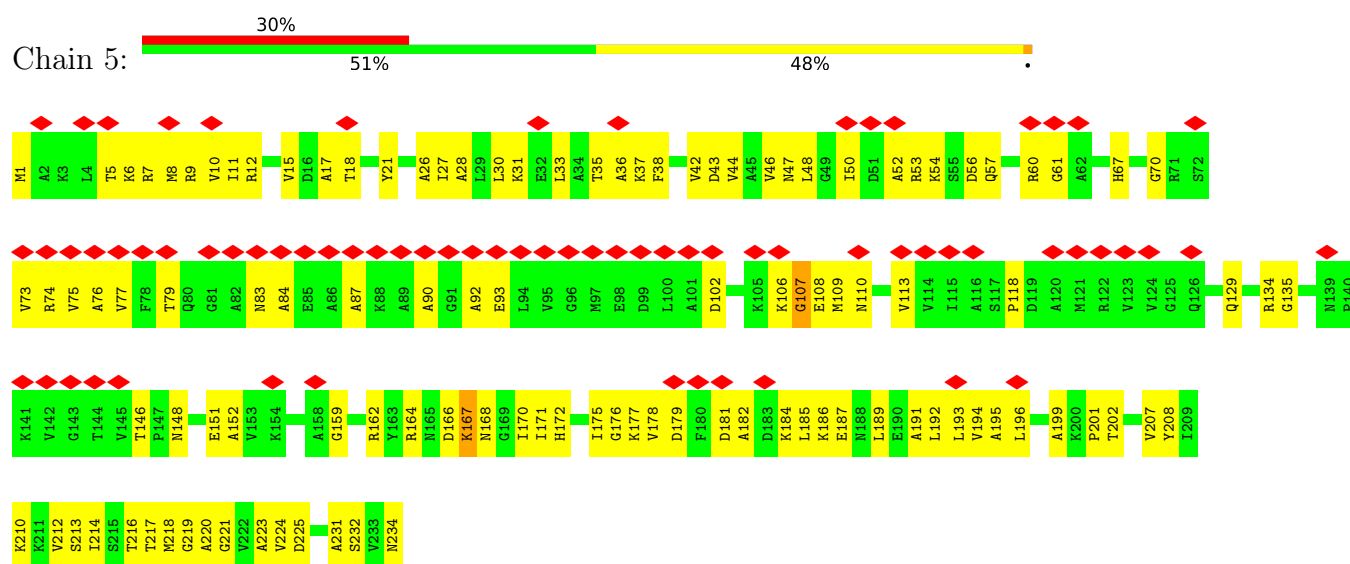
- Molecule 24: 50S ribosomal protein L35



- Molecule 25: 50S ribosomal protein L36



- Molecule 26: 50S ribosomal protein L1



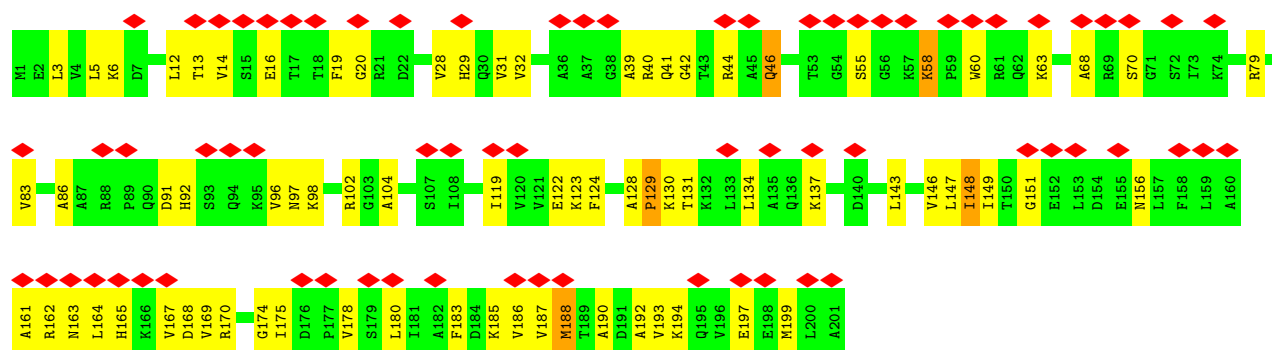
• Molecule 27: 50S ribosomal protein L2



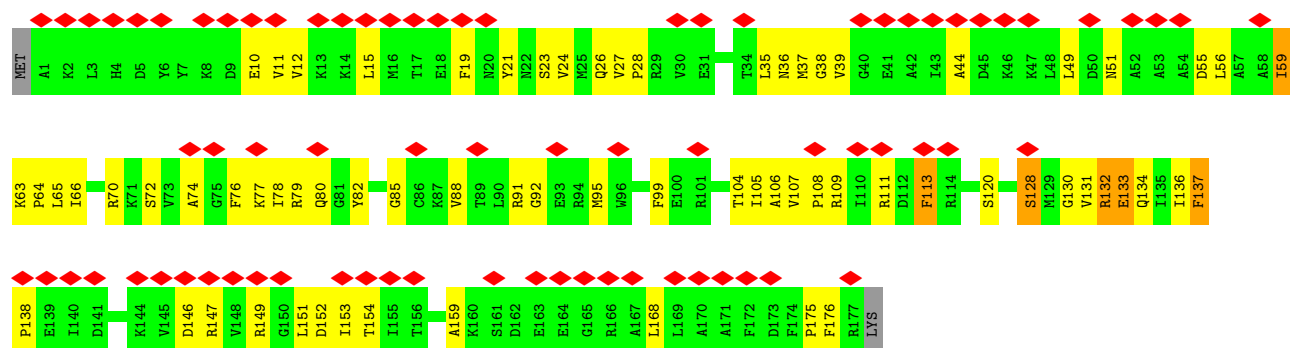
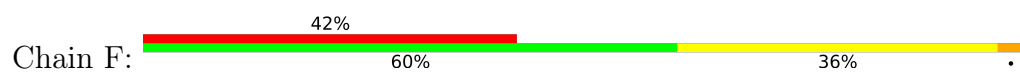
• Molecule 28: 50S ribosomal protein L3



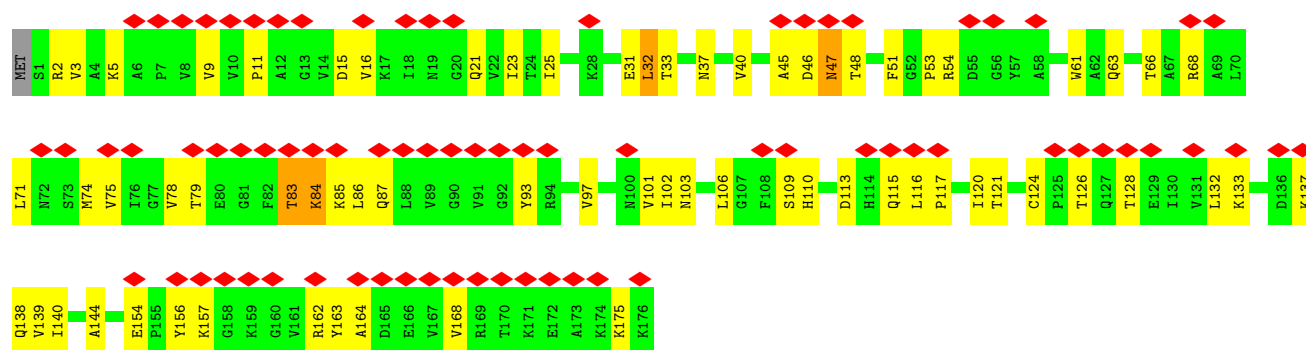
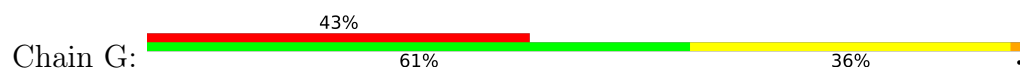
• Molecule 29: 50S ribosomal protein L4



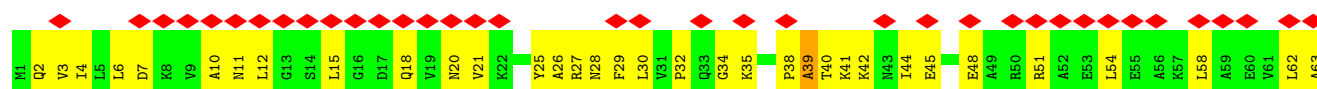
• Molecule 30: 50S ribosomal protein L5

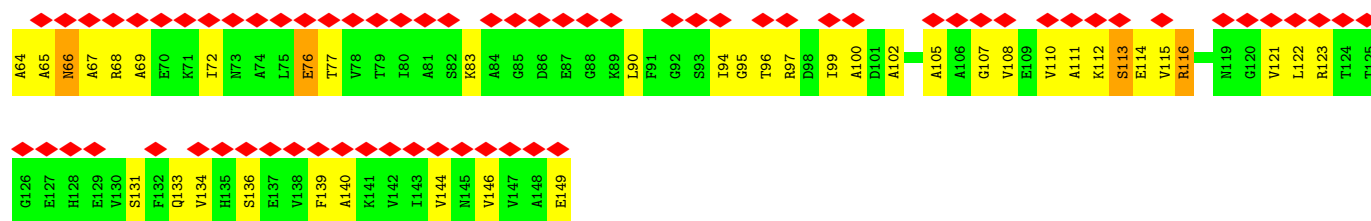


• Molecule 31: 50S ribosomal protein L6

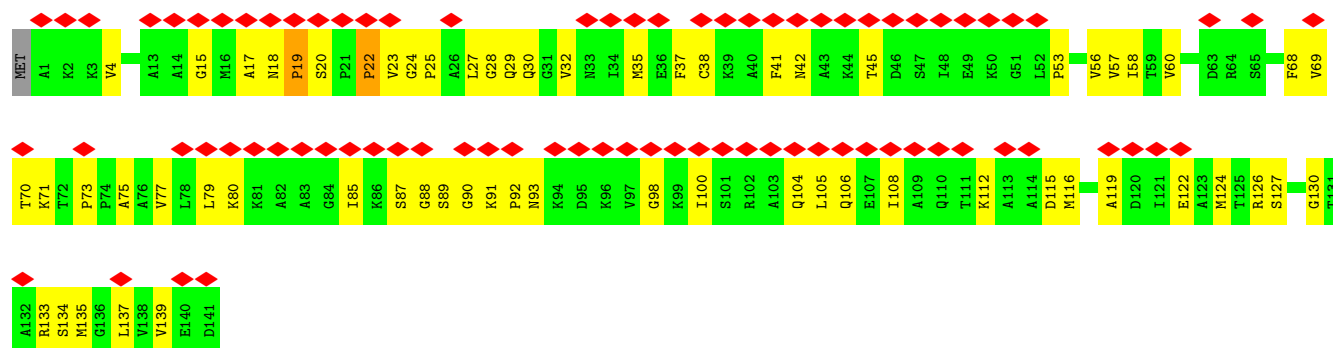


• Molecule 32: 50S ribosomal protein L9

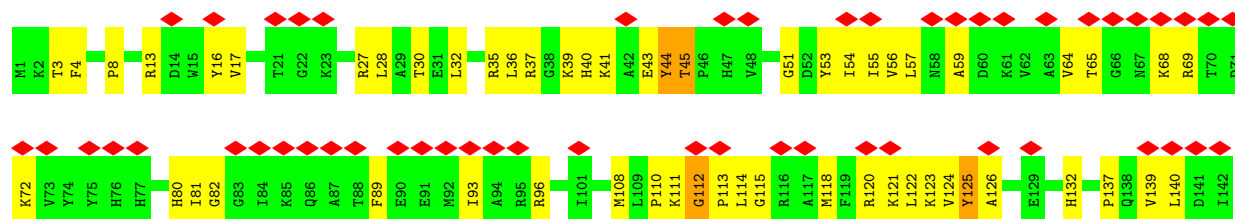




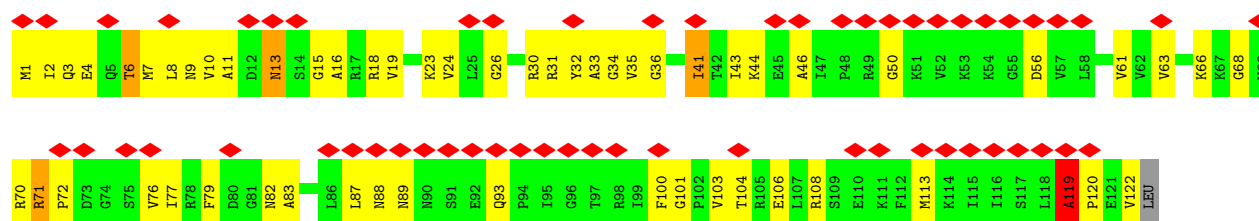
• Molecule 33: 50S ribosomal protein L11



• Molecule 34: 50S ribosomal protein L13

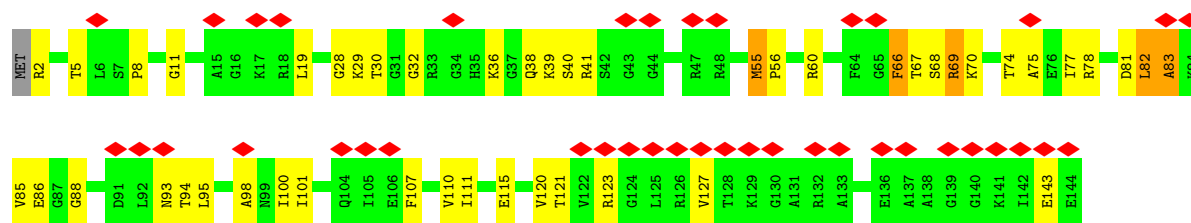


• Molecule 35: 50S ribosomal protein L14

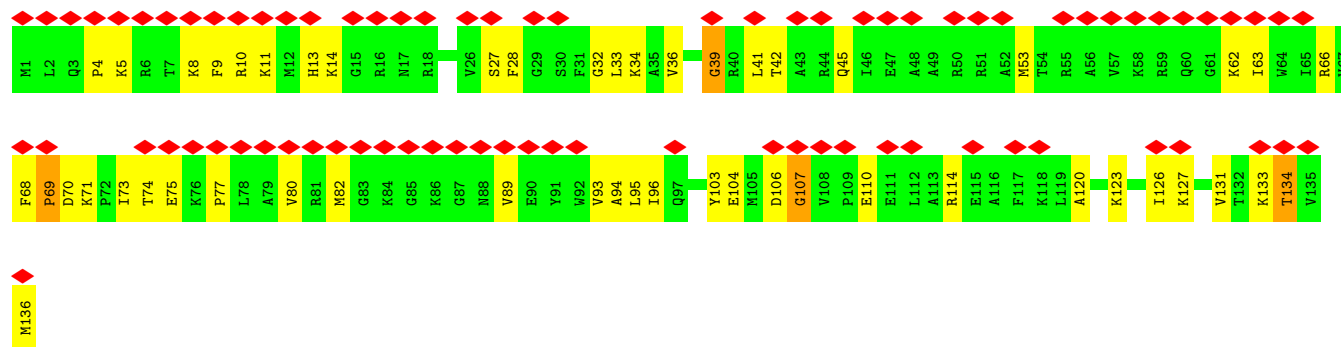


• Molecule 36: 50S ribosomal protein L15

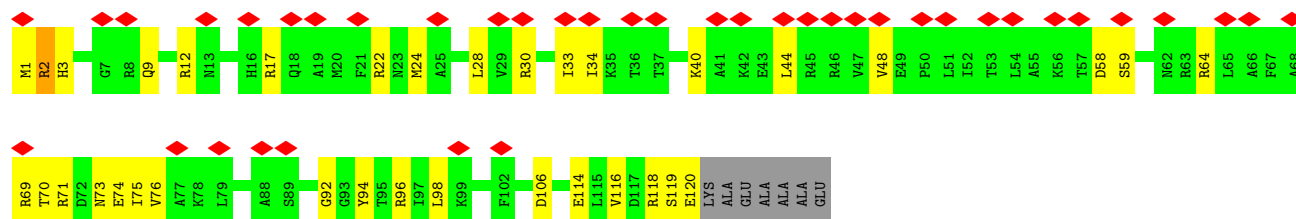




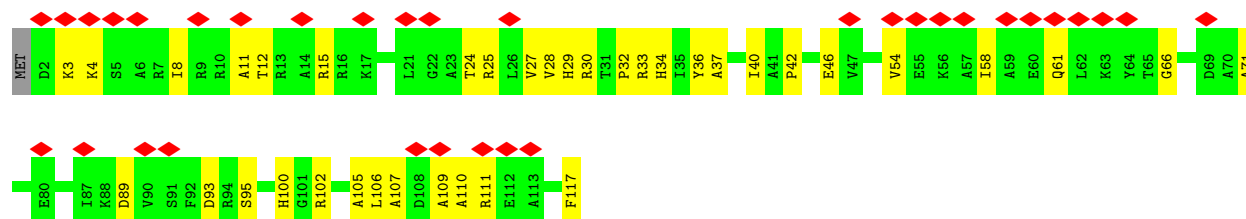
• Molecule 37: 50S ribosomal protein L16



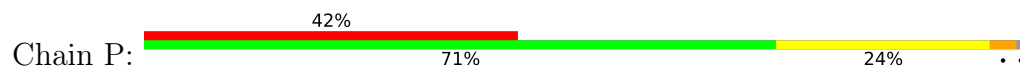
• Molecule 38: 50S ribosomal protein L17

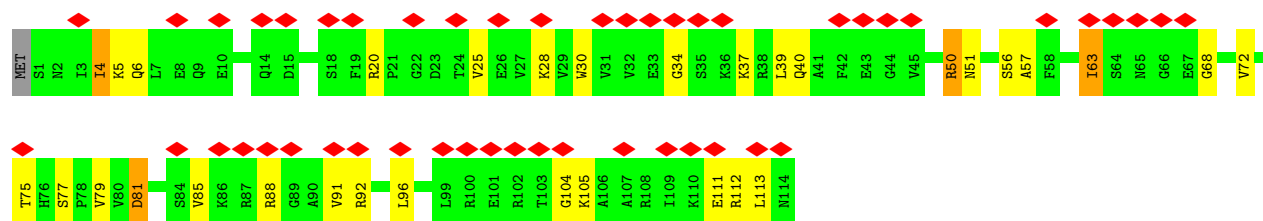


• Molecule 39: 50S ribosomal protein L18

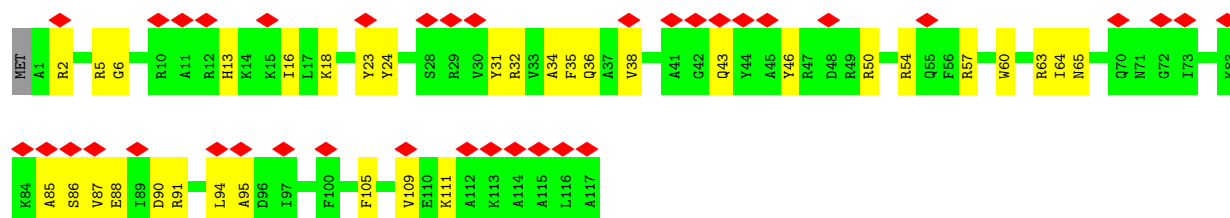


• Molecule 40: 50S ribosomal protein L19

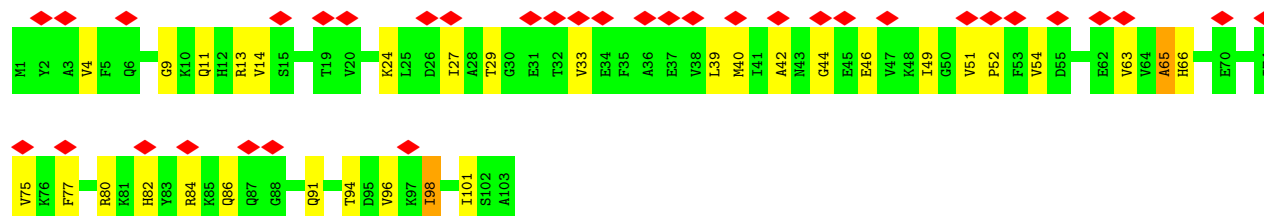




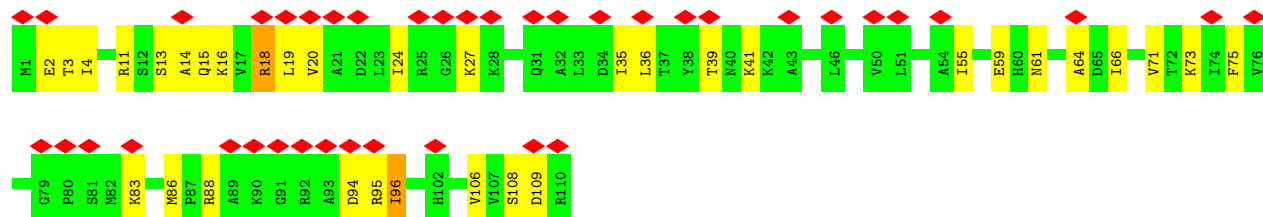
• Molecule 41: 50S ribosomal protein L20



• Molecule 42: 50S ribosomal protein L21

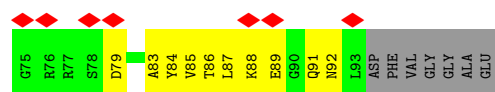


• Molecule 43: 50S ribosomal protein L22

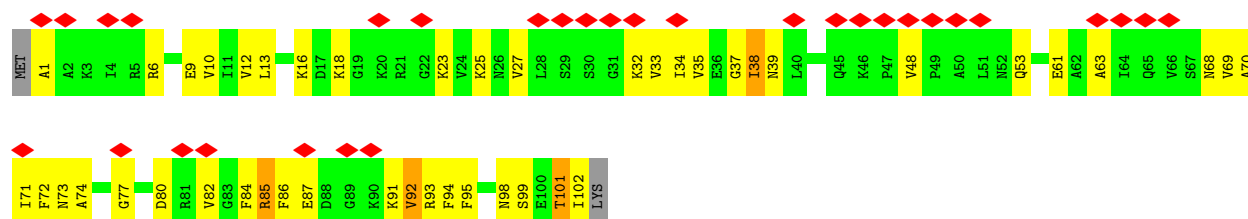


• Molecule 44: 50S ribosomal protein L23

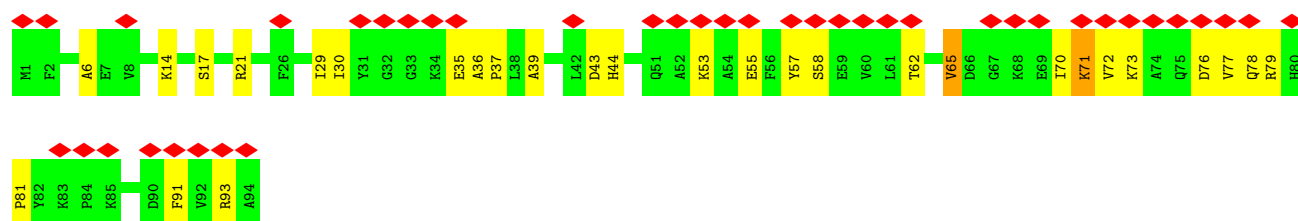




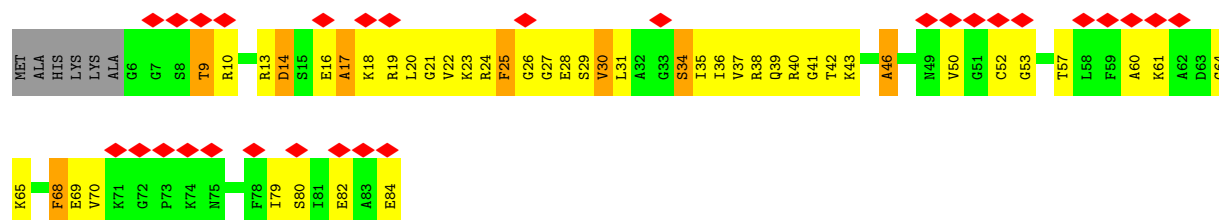
- Molecule 45: 50S ribosomal protein L24



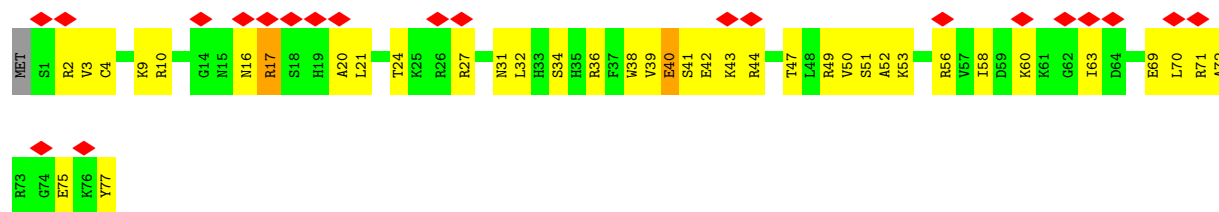
- Molecule 46: 50S ribosomal protein L25



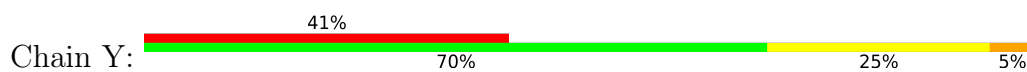
- Molecule 47: 50S ribosomal protein L27



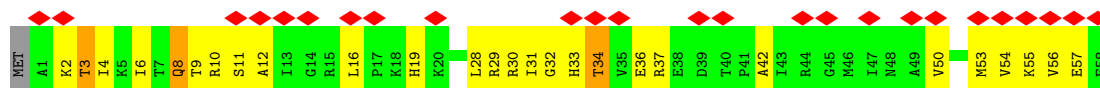
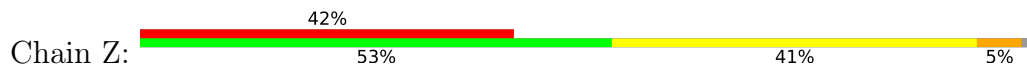
- Molecule 48: 50S ribosomal protein L28



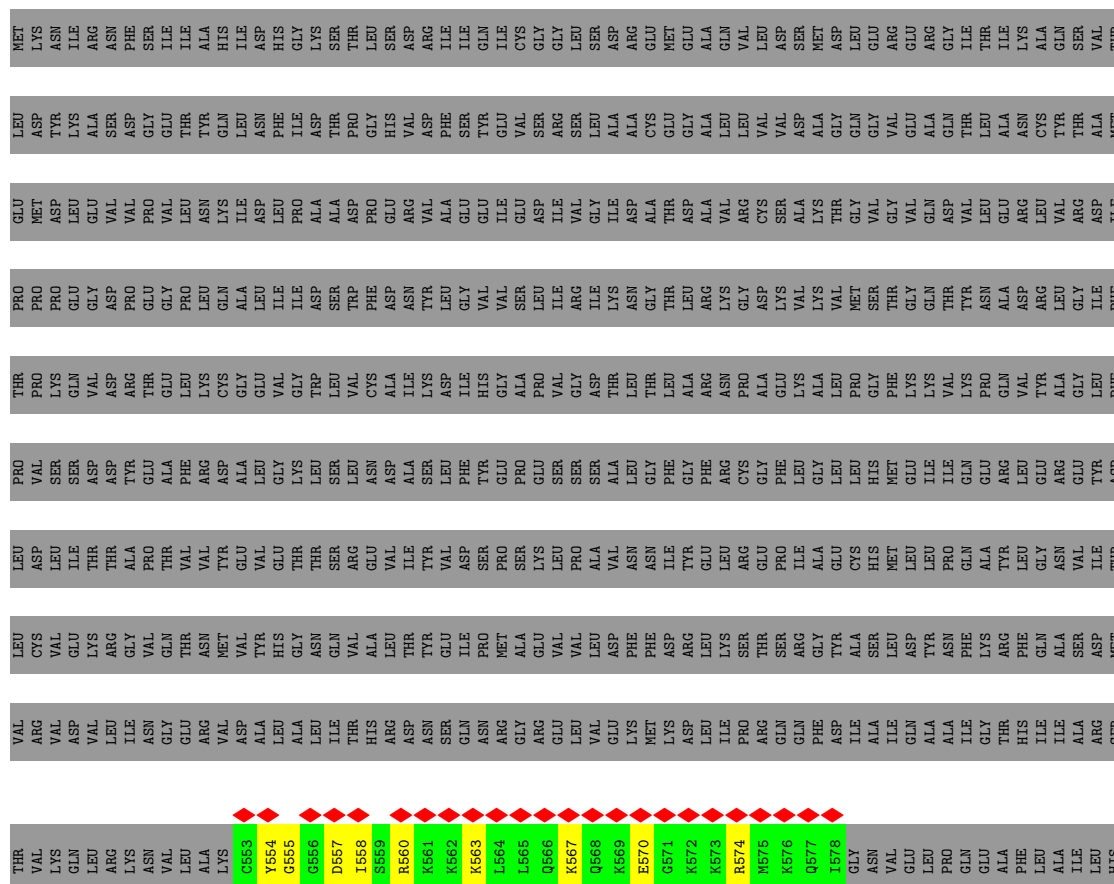
- Molecule 49: 50S ribosomal protein L29



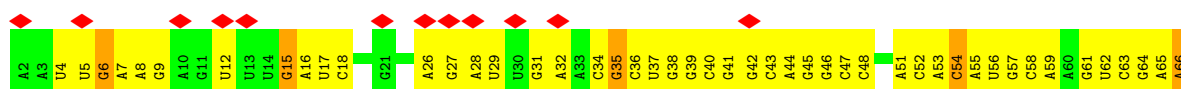
- Molecule 50: 50S ribosomal protein L30

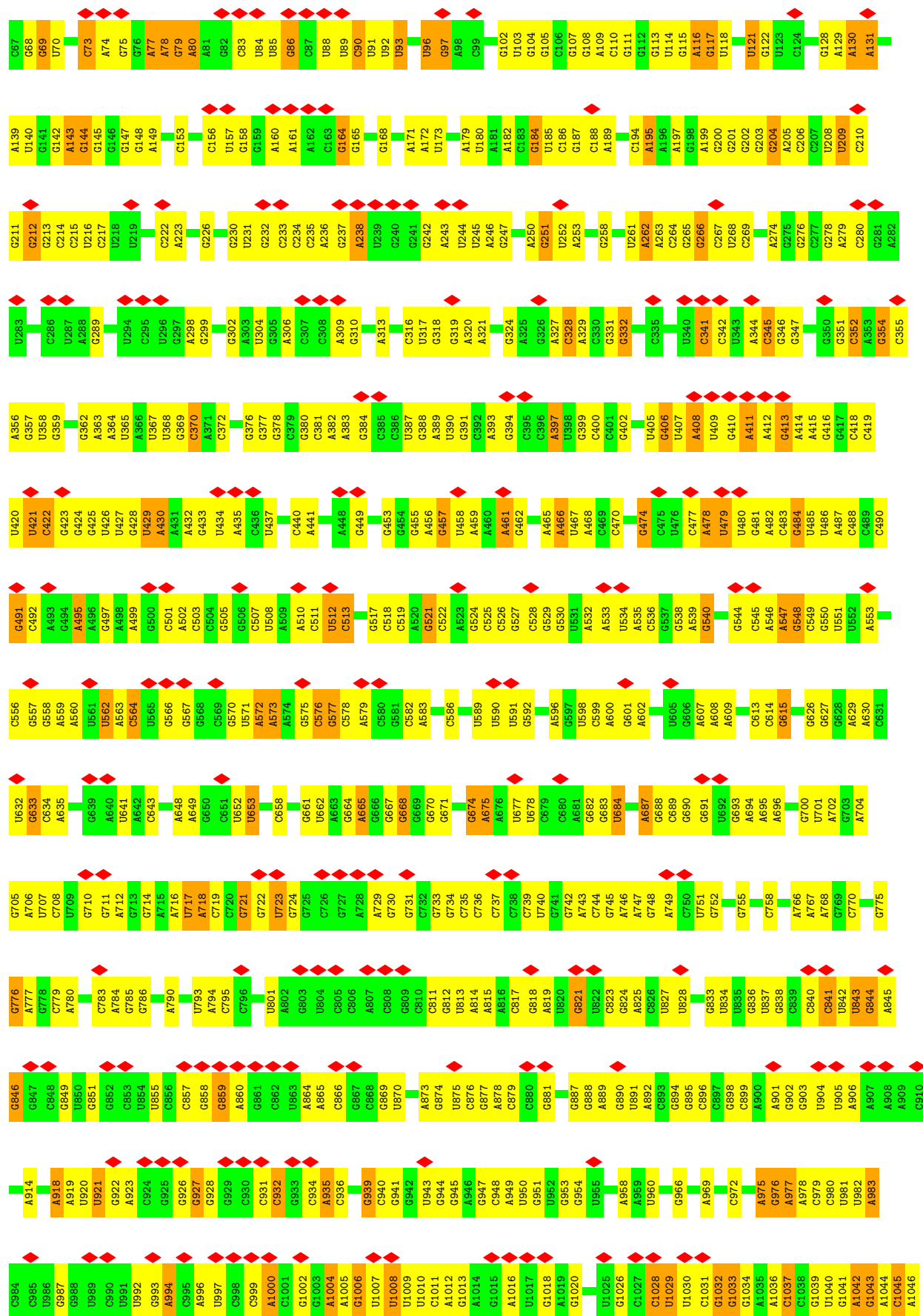


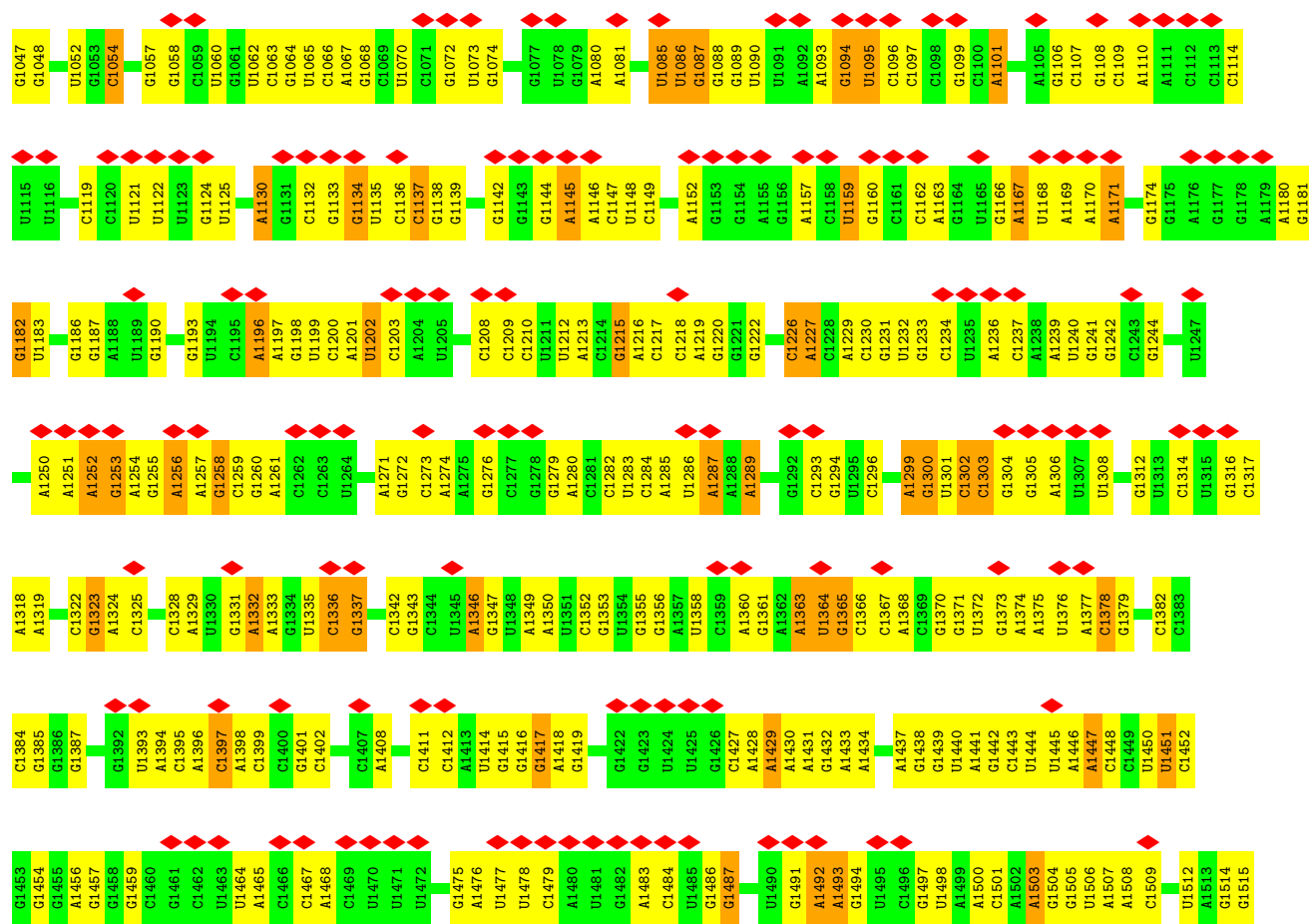
- Molecule 51: Elongation factor 4



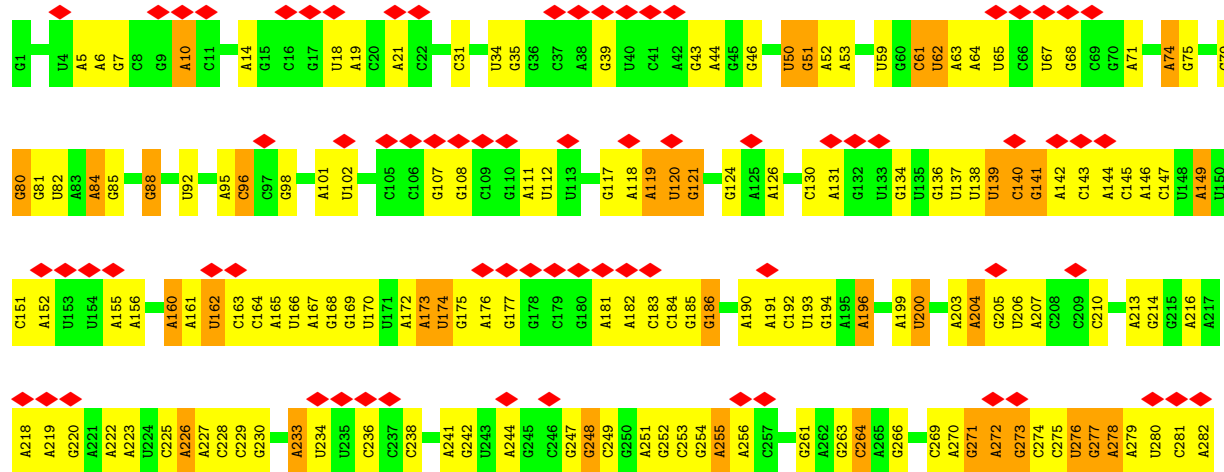
- Molecule 52: 16S ribosomal RNA

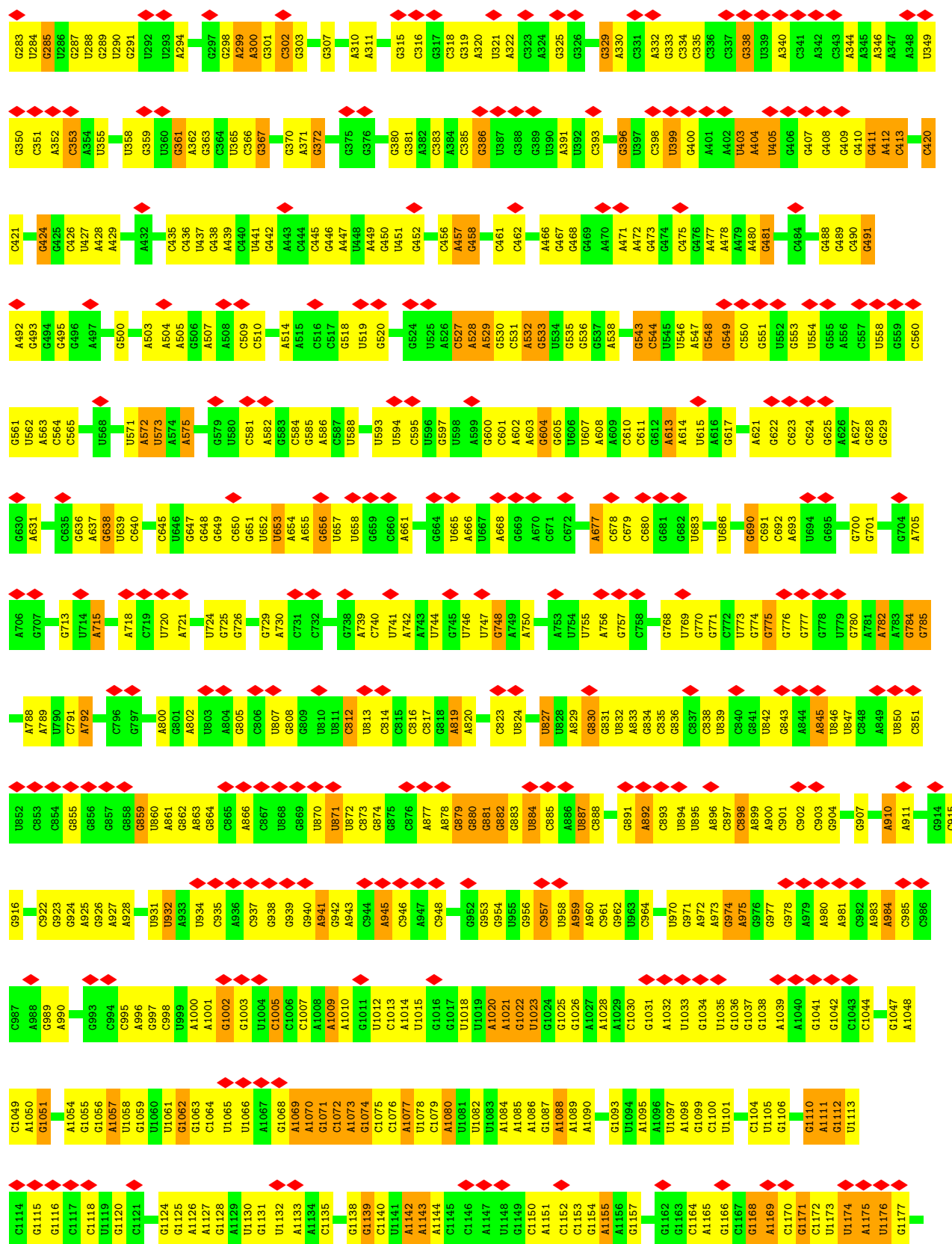




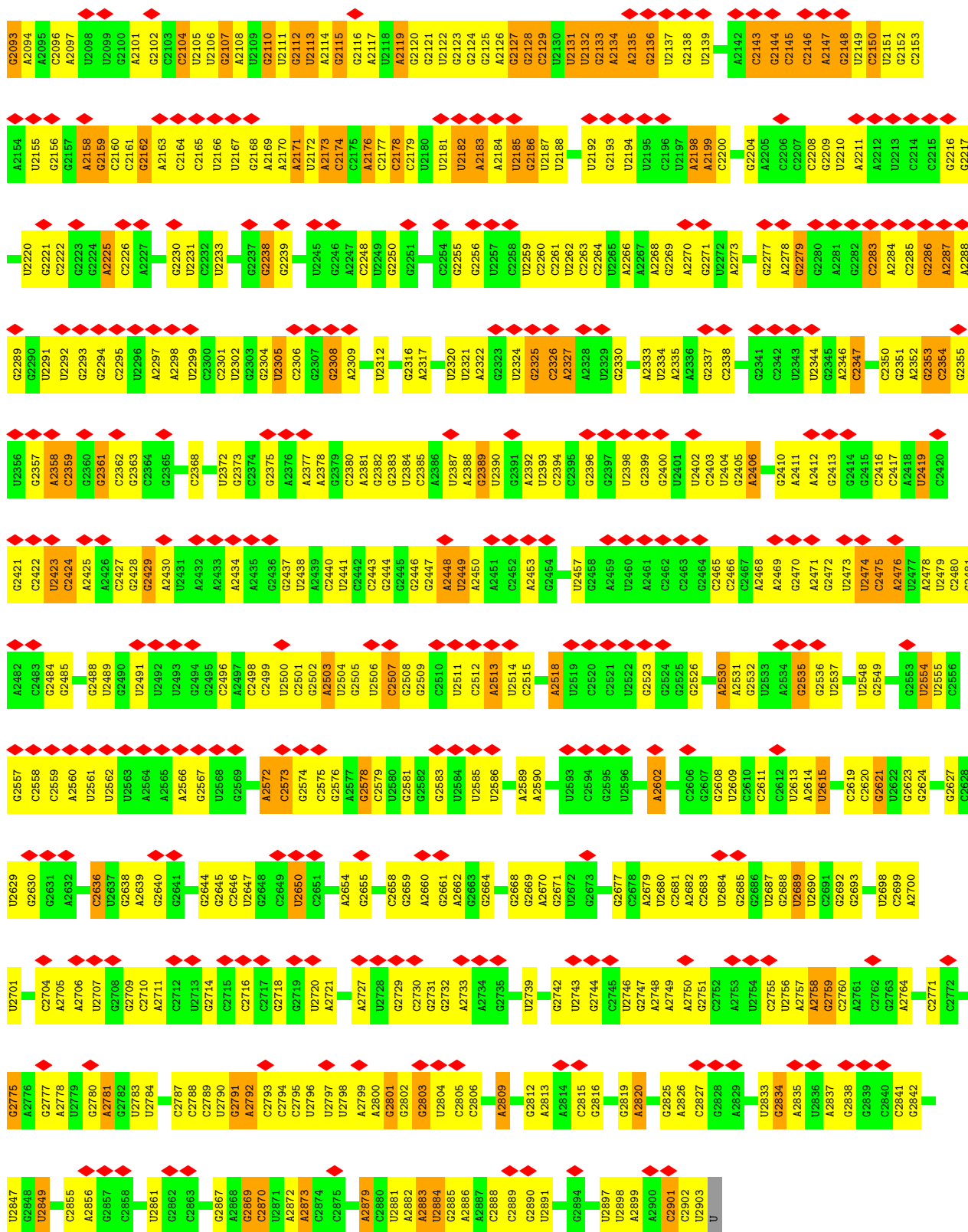


• Molecule 53: 23S ribosomal RNA



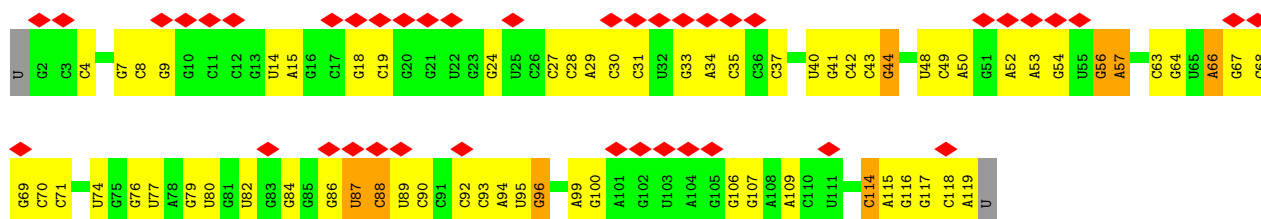




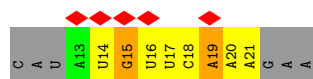


• Molecule 54: 5S ribosomal RNA

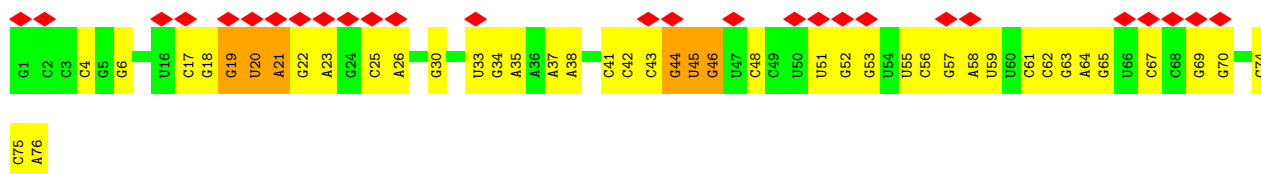
Chain B: 34% 42% 49% 7%



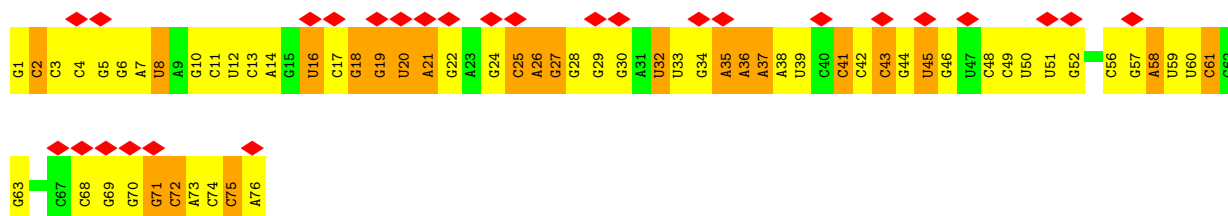
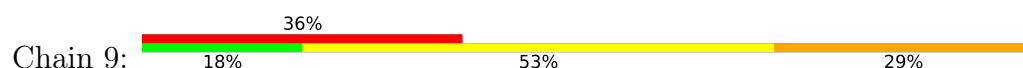
• Molecule 55: mRNA



• Molecule 56: tRNA



• Molecule 56: tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18772	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
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	0.028	Depositor
Minimum map value	-0.010	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0035	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.41	0/1735	0.89	5/2338 (0.2%)
2	c	0.44	0/1651	0.80	0/2225
3	d	0.43	0/1665	0.81	0/2227
4	e	0.49	0/1118	0.88	0/1504
5	f	0.43	0/851	0.89	1/1150 (0.1%)
6	g	0.45	0/1195	0.85	2/1602 (0.1%)
7	h	0.48	0/989	0.87	2/1326 (0.2%)
8	i	0.42	0/1034	0.83	0/1375
9	j	0.42	0/796	0.92	1/1077 (0.1%)
10	k	0.49	0/893	0.95	6/1205 (0.5%)
11	l	0.44	0/969	0.93	3/1300 (0.2%)
12	m	0.46	0/892	0.90	1/1193 (0.1%)
13	n	0.43	0/785	0.87	2/1043 (0.2%)
14	o	0.45	0/722	0.72	0/964
15	p	0.42	0/659	0.84	2/884 (0.2%)
16	q	0.40	0/657	0.82	0/881
17	r	0.46	0/462	0.78	1/621 (0.2%)
18	s	0.38	0/652	0.90	0/877
19	t	0.52	0/671	0.82	0/888
20	u	0.45	0/430	0.87	2/570 (0.4%)
21	0	0.47	0/450	0.82	1/599 (0.2%)
22	1	0.43	0/416	0.96	2/554 (0.4%)
23	2	0.50	0/380	0.82	2/498 (0.4%)
24	3	0.52	0/513	0.85	0/676
25	4	0.45	0/303	1.03	4/397 (1.0%)
26	5	0.40	0/1748	0.98	8/2355 (0.3%)
27	C	0.51	0/2115	0.95	6/2844 (0.2%)
28	D	0.49	0/1586	0.93	3/2134 (0.1%)
29	E	0.45	0/1571	0.84	3/2113 (0.1%)
30	F	0.43	0/1434	0.89	3/1926 (0.2%)
31	G	0.42	0/1343	0.87	1/1816 (0.1%)
32	H	0.42	0/1122	0.91	2/1515 (0.1%)
33	I	0.41	0/1046	0.92	2/1410 (0.1%)
34	J	0.50	0/1152	0.87	2/1551 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	K	0.54	0/947	0.95	5/1268 (0.4%)
36	L	0.45	0/1054	0.95	3/1403 (0.2%)
37	M	0.49	0/1093	0.89	3/1460 (0.2%)
38	N	0.51	0/973	0.82	0/1301
39	O	0.43	0/902	0.78	0/1209
40	P	0.46	0/929	0.88	1/1242 (0.1%)
41	Q	0.53	0/960	0.77	0/1278
42	R	0.41	0/829	0.84	2/1107 (0.2%)
43	S	0.51	0/864	0.92	2/1156 (0.2%)
44	T	0.48	0/744	1.01	2/994 (0.2%)
45	U	0.43	0/787	0.89	0/1051
46	V	0.42	0/766	0.84	0/1025
47	W	0.48	0/603	0.96	1/797 (0.1%)
48	X	0.47	0/635	0.84	0/848
49	Y	0.45	0/510	0.77	0/677
50	Z	0.45	0/453	0.93	1/605 (0.2%)
51	x	0.34	0/214	0.76	0/275
52	a	0.24	0/36834	0.28	0/57462
53	A	0.27	0/69799	0.29	0/108892
54	B	0.21	0/2828	0.26	0/4410
55	7	0.23	0/213	0.32	0/329
56	8	0.22	0/1813	0.33	0/2823
56	9	0.17	0/1813	0.32	0/2823
All	All	0.33	0/160568	0.52	87/240073 (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
20	u	0	1
31	G	0	1
35	K	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 87 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	D	151	THR	CA-C-N	-8.33	109.42	119.84
28	D	151	THR	C-N-CA	-8.33	109.42	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	J	112	GLY	CA-C-N	7.88	129.70	119.84
34	J	112	GLY	C-N-CA	7.88	129.70	119.84
6	g	70	ARG	CA-C-N	7.88	127.81	119.85

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
31	G	83	THR	Peptide
35	K	71	ARG	Peptide
20	u	39	GLU	Peptide

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	1704	0	1732	58	0
2	c	1624	0	1696	41	0
3	d	1643	0	1707	80	0
4	e	1105	0	1148	38	0
5	f	832	0	824	23	0
6	g	1181	0	1238	44	0
7	h	979	0	1031	45	0
8	i	1022	0	1070	57	0
9	j	786	0	828	33	0
10	k	877	0	887	38	0
11	l	955	0	1016	53	0
12	m	883	0	941	39	0
13	n	774	0	824	44	0
14	o	714	0	734	28	0
15	p	649	0	666	28	0
16	q	648	0	691	19	0
17	r	455	0	478	17	0
18	s	637	0	665	19	0
19	t	665	0	714	23	0
20	u	425	0	449	17	0
21	0	444	0	461	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	1	409	0	440	19	0
23	2	377	0	418	6	0
24	3	504	0	574	14	0
25	4	302	0	340	17	0
26	5	1733	0	1824	101	0
27	C	2076	0	2152	72	0
28	D	1565	0	1616	56	0
29	E	1552	0	1619	50	0
30	F	1410	0	1447	53	0
31	G	1323	0	1374	50	0
32	H	1111	0	1148	49	0
33	I	1032	0	1088	53	0
34	J	1129	0	1162	50	0
35	K	938	0	1012	37	0
36	L	1045	0	1117	26	0
37	M	1074	0	1157	36	0
38	N	960	0	1000	28	0
39	O	892	0	923	29	0
40	P	917	0	965	23	0
41	Q	947	0	1022	36	0
42	R	816	0	839	21	0
43	S	857	0	922	24	0
44	T	738	0	807	29	0
45	U	779	0	834	29	0
46	V	753	0	780	21	0
47	W	596	0	610	52	0
48	X	625	0	655	33	0
49	Y	509	0	543	12	0
50	Z	449	0	491	21	0
51	x	214	0	244	8	0
52	a	32895	0	16553	712	0
53	A	62320	0	31343	1197	0
54	B	2529	0	1281	50	0
55	7	191	0	97	8	0
56	8	1623	0	821	51	0
56	9	1623	0	821	99	0
All	All	147815	0	99839	3446	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 3446 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)
53:A:271:G:C5	53:A:367:G:C2	1.87	1.62
53:A:271:G:C8	53:A:367:G:N2	1.70	1.54
53:A:271:G:N7	53:A:367:G:C2	1.77	1.45
53:A:271:G:N7	53:A:367:G:N1	1.67	1.40
53:A:272:A:C2	53:A:273:G:C5	2.10	1.39

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	b	216/241 (90%)	181 (84%)	23 (11%)	12 (6%)	1	16
2	c	204/233 (88%)	190 (93%)	7 (3%)	7 (3%)	3	25
3	d	203/206 (98%)	179 (88%)	15 (7%)	9 (4%)	2	19
4	e	148/167 (89%)	128 (86%)	15 (10%)	5 (3%)	3	25
5	f	100/135 (74%)	79 (79%)	13 (13%)	8 (8%)	1	9
6	g	149/179 (83%)	125 (84%)	18 (12%)	6 (4%)	2	21
7	h	127/130 (98%)	115 (91%)	11 (9%)	1 (1%)	16	48
8	i	125/130 (96%)	109 (87%)	12 (10%)	4 (3%)	3	25
9	j	96/103 (93%)	78 (81%)	13 (14%)	5 (5%)	1	17
10	k	115/129 (89%)	104 (90%)	8 (7%)	3 (3%)	4	28
11	l	121/124 (98%)	105 (87%)	14 (12%)	2 (2%)	7	34
12	m	112/118 (95%)	103 (92%)	5 (4%)	4 (4%)	2	23
13	n	92/101 (91%)	77 (84%)	8 (9%)	7 (8%)	1	10
14	o	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	10	40
15	p	80/82 (98%)	70 (88%)	8 (10%)	2 (2%)	4	29
16	q	78/84 (93%)	65 (83%)	8 (10%)	5 (6%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	r	53/75 (71%)	51 (96%)	1 (2%)	1 (2%)	6	33
18	s	77/92 (84%)	68 (88%)	6 (8%)	3 (4%)	2	21
19	t	83/87 (95%)	80 (96%)	1 (1%)	2 (2%)	4	29
20	u	49/71 (69%)	36 (74%)	10 (20%)	3 (6%)	1	14
21	0	54/57 (95%)	49 (91%)	2 (4%)	3 (6%)	1	16
22	1	48/55 (87%)	43 (90%)	3 (6%)	2 (4%)	2	20
23	2	44/46 (96%)	39 (89%)	3 (7%)	2 (4%)	2	18
24	3	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	35
25	4	36/38 (95%)	29 (81%)	2 (6%)	5 (14%)	0	3
26	5	232/234 (99%)	198 (85%)	32 (14%)	2 (1%)	14	45
27	C	268/273 (98%)	233 (87%)	20 (8%)	15 (6%)	1	16
28	D	207/209 (99%)	168 (81%)	28 (14%)	11 (5%)	1	16
29	E	199/201 (99%)	170 (85%)	18 (9%)	11 (6%)	1	16
30	F	175/179 (98%)	153 (87%)	13 (7%)	9 (5%)	1	17
31	G	174/177 (98%)	142 (82%)	24 (14%)	8 (5%)	2	18
32	H	147/149 (99%)	114 (78%)	22 (15%)	11 (8%)	1	11
33	I	139/142 (98%)	121 (87%)	13 (9%)	5 (4%)	2	23
34	J	140/142 (99%)	120 (86%)	13 (9%)	7 (5%)	1	17
35	K	120/123 (98%)	96 (80%)	17 (14%)	7 (6%)	1	15
36	L	141/144 (98%)	115 (82%)	14 (10%)	12 (8%)	0	8
37	M	134/136 (98%)	114 (85%)	13 (10%)	7 (5%)	1	17
38	N	118/127 (93%)	105 (89%)	10 (8%)	3 (2%)	4	29
39	O	114/117 (97%)	105 (92%)	7 (6%)	2 (2%)	6	34
40	P	112/115 (97%)	98 (88%)	8 (7%)	6 (5%)	1	16
41	Q	115/118 (98%)	109 (95%)	5 (4%)	1 (1%)	14	45
42	R	101/103 (98%)	86 (85%)	11 (11%)	4 (4%)	2	21
43	S	108/110 (98%)	93 (86%)	9 (8%)	6 (6%)	1	16
44	T	91/100 (91%)	65 (71%)	17 (19%)	9 (10%)	0	6
45	U	100/104 (96%)	79 (79%)	13 (13%)	8 (8%)	1	9
46	V	92/94 (98%)	84 (91%)	6 (6%)	2 (2%)	5	31
47	W	77/85 (91%)	55 (71%)	13 (17%)	9 (12%)	0	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	X	75/78 (96%)	65 (87%)	7 (9%)	3 (4%)	2	21
49	Y	61/63 (97%)	51 (84%)	7 (12%)	3 (5%)	1	17
50	Z	56/59 (95%)	48 (86%)	6 (11%)	2 (4%)	2	23
51	x	24/599 (4%)	23 (96%)	1 (4%)	0	100	100
All	All	5878/6817 (86%)	5045 (86%)	567 (10%)	266 (4%)	3	18

5 of 266 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	72	LYS
1	b	163	ILE
3	d	151	LYS
5	f	63	ASN
5	f	93	LYS

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	180/199 (90%)	180 (100%)	0	100	100
2	c	170/190 (90%)	170 (100%)	0	100	100
3	d	172/173 (99%)	172 (100%)	0	100	100
4	e	113/126 (90%)	113 (100%)	0	100	100
5	f	89/116 (77%)	89 (100%)	0	100	100
6	g	124/147 (84%)	124 (100%)	0	100	100
7	h	104/105 (99%)	104 (100%)	0	100	100
8	i	105/107 (98%)	105 (100%)	0	100	100
9	j	86/90 (96%)	86 (100%)	0	100	100
10	k	90/99 (91%)	90 (100%)	0	100	100
11	l	103/104 (99%)	103 (100%)	0	100	100
12	m	92/96 (96%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	n	79/84 (94%)	79 (100%)	0	100	100
14	o	76/77 (99%)	76 (100%)	0	100	100
15	p	65/65 (100%)	65 (100%)	0	100	100
16	q	74/78 (95%)	74 (100%)	0	100	100
17	r	48/65 (74%)	48 (100%)	0	100	100
18	s	70/79 (89%)	70 (100%)	0	100	100
19	t	65/66 (98%)	65 (100%)	0	100	100
20	u	44/61 (72%)	44 (100%)	0	100	100
21	0	47/48 (98%)	47 (100%)	0	100	100
22	1	45/49 (92%)	45 (100%)	0	100	100
23	2	38/38 (100%)	38 (100%)	0	100	100
24	3	51/51 (100%)	51 (100%)	0	100	100
25	4	34/34 (100%)	34 (100%)	0	100	100
26	5	181/181 (100%)	181 (100%)	0	100	100
27	C	215/218 (99%)	215 (100%)	0	100	100
28	D	164/164 (100%)	164 (100%)	0	100	100
29	E	165/165 (100%)	165 (100%)	0	100	100
30	F	148/150 (99%)	148 (100%)	0	100	100
31	G	137/138 (99%)	137 (100%)	0	100	100
32	H	114/114 (100%)	114 (100%)	0	100	100
33	I	109/110 (99%)	109 (100%)	0	100	100
34	J	116/116 (100%)	116 (100%)	0	100	100
35	K	103/104 (99%)	103 (100%)	0	100	100
36	L	102/103 (99%)	102 (100%)	0	100	100
37	M	109/109 (100%)	109 (100%)	0	100	100
38	N	100/103 (97%)	100 (100%)	0	100	100
39	O	86/87 (99%)	86 (100%)	0	100	100
40	P	99/100 (99%)	99 (100%)	0	100	100
41	Q	89/90 (99%)	89 (100%)	0	100	100
42	R	84/84 (100%)	84 (100%)	0	100	100
43	S	93/93 (100%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	T	80/84 (95%)	79 (99%)	1 (1%)	61	71
45	U	83/85 (98%)	83 (100%)	0	100	100
46	V	78/78 (100%)	78 (100%)	0	100	100
47	W	59/63 (94%)	59 (100%)	0	100	100
48	X	67/68 (98%)	67 (100%)	0	100	100
49	Y	55/55 (100%)	55 (100%)	0	100	100
50	Z	48/49 (98%)	48 (100%)	0	100	100
51	x	23/511 (4%)	23 (100%)	0	100	100
All	All	4871/5569 (88%)	4870 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	T	43	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

Mol	Chain	Res	Type
35	K	93	GLN
49	Y	41	HIS
39	O	29	HIS
42	R	66	HIS
21	0	5	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	a	1532/1533 (99%)	301 (19%)	0
53	A	2902/2904 (99%)	597 (20%)	16 (0%)
54	B	117/120 (97%)	21 (17%)	0
55	7	8/15 (53%)	4 (50%)	0
56	8	75/76 (98%)	8 (10%)	2 (2%)
56	9	75/76 (98%)	33 (44%)	1 (1%)
All	All	4709/4724 (99%)	964 (20%)	19 (0%)

5 of 964 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	a	4	U
52	a	6	G
52	a	9	G
52	a	12	U
52	a	15	G

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	A	2423	U
56	8	45	U
56	9	71	G
56	8	20	U
53	A	1020	A

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 [i](#)

There are no chain breaks in this entry.

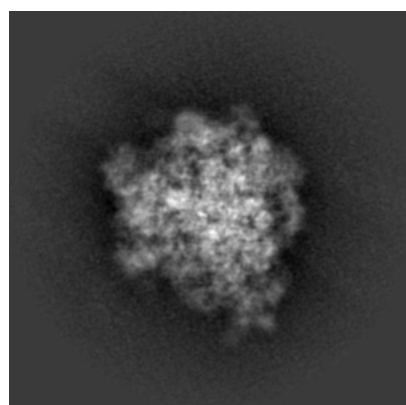
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6549. These allow visual inspection of the internal detail of the map and identification of artifacts.

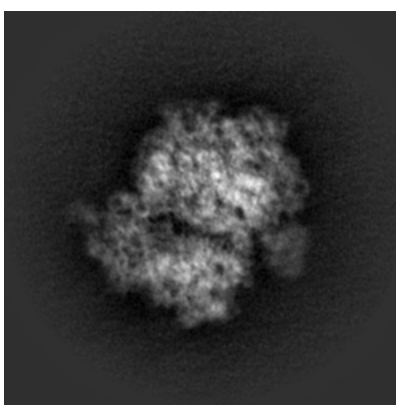
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

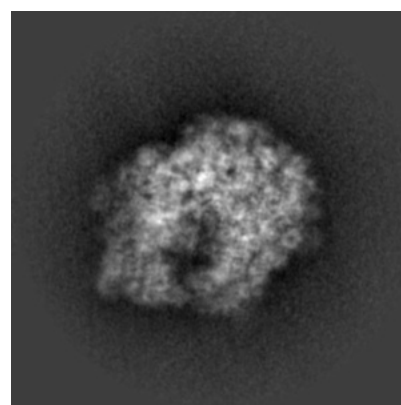
6.1.1 Primary map



X



Y

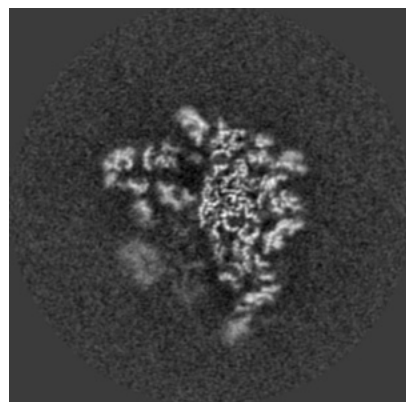


Z

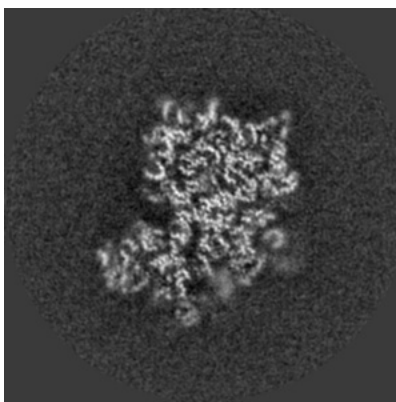
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

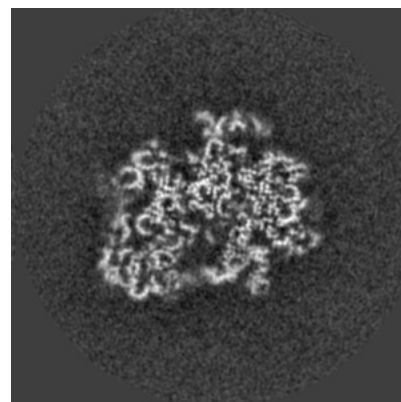
6.2.1 Primary map



X Index: 160



Y Index: 160

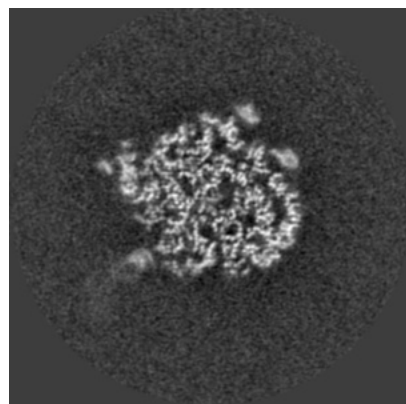


Z Index: 160

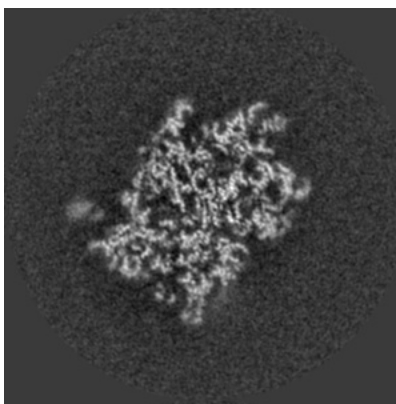
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

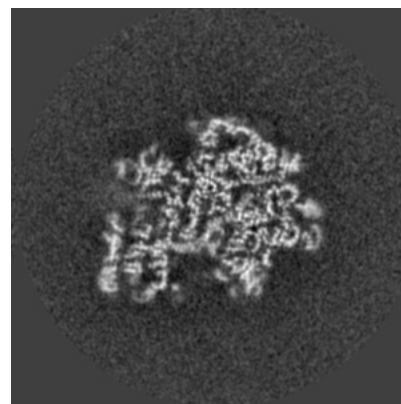
6.3.1 Primary map



X Index: 185



Y Index: 178

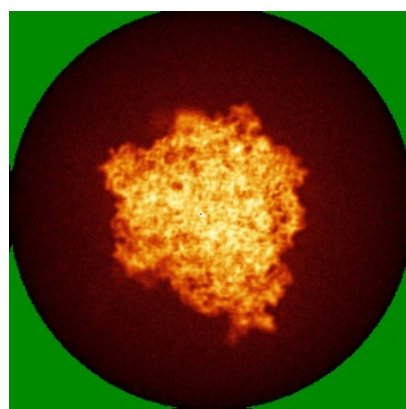


Z Index: 167

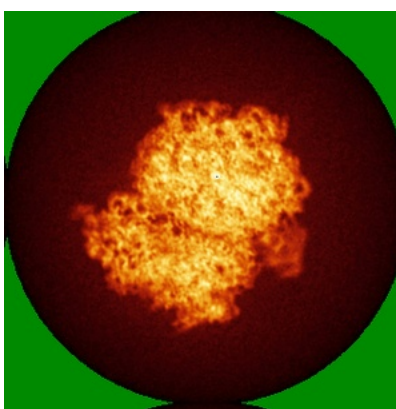
The images above show the largest variance slices of the map in three orthogonal directions.

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

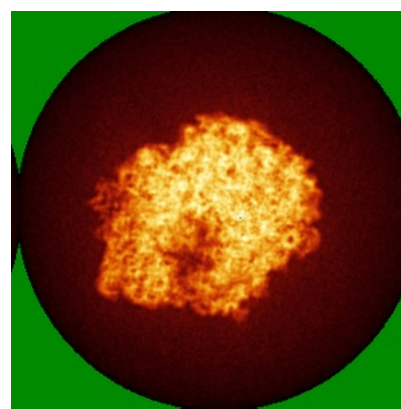
6.4.1 Primary map



X



Y

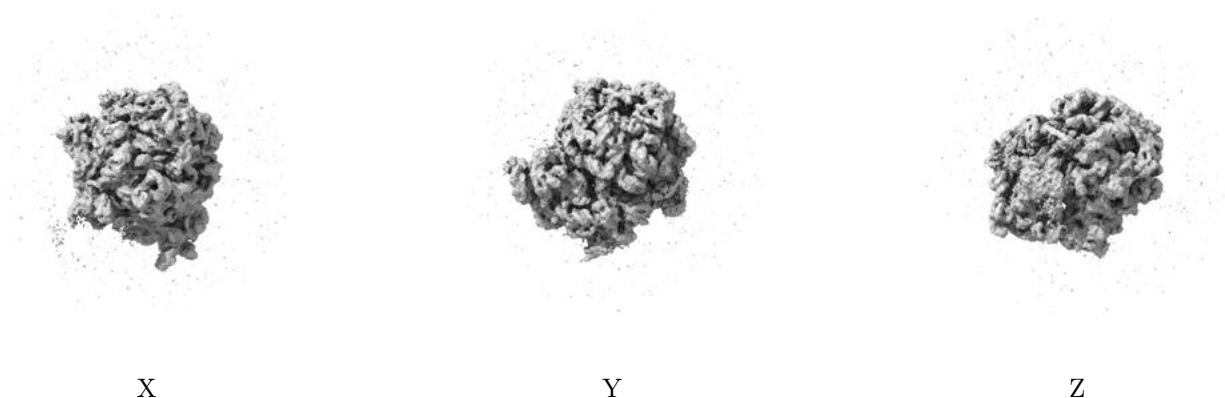


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

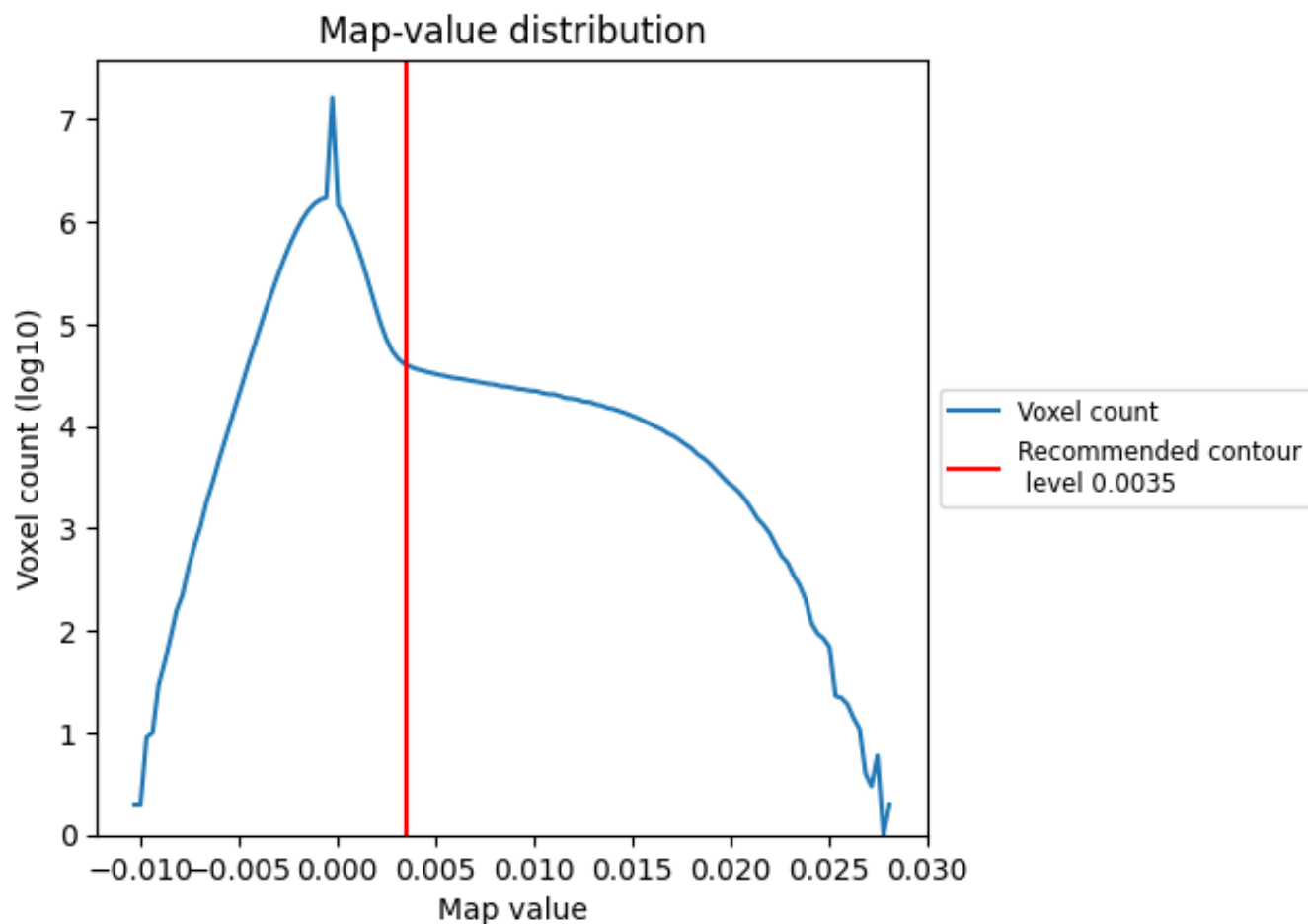
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

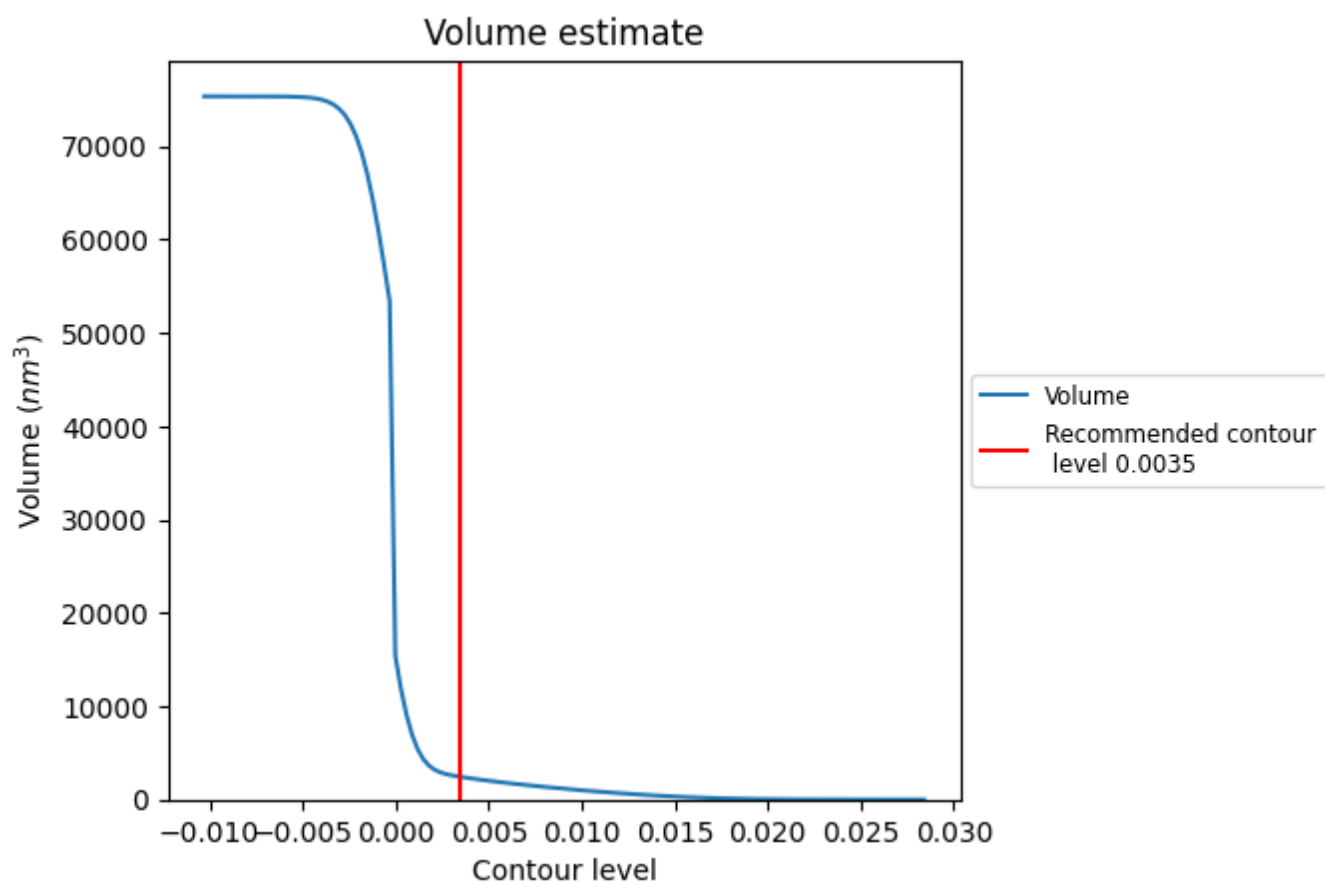
This section contains the results of statistical analysis of the map.

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.

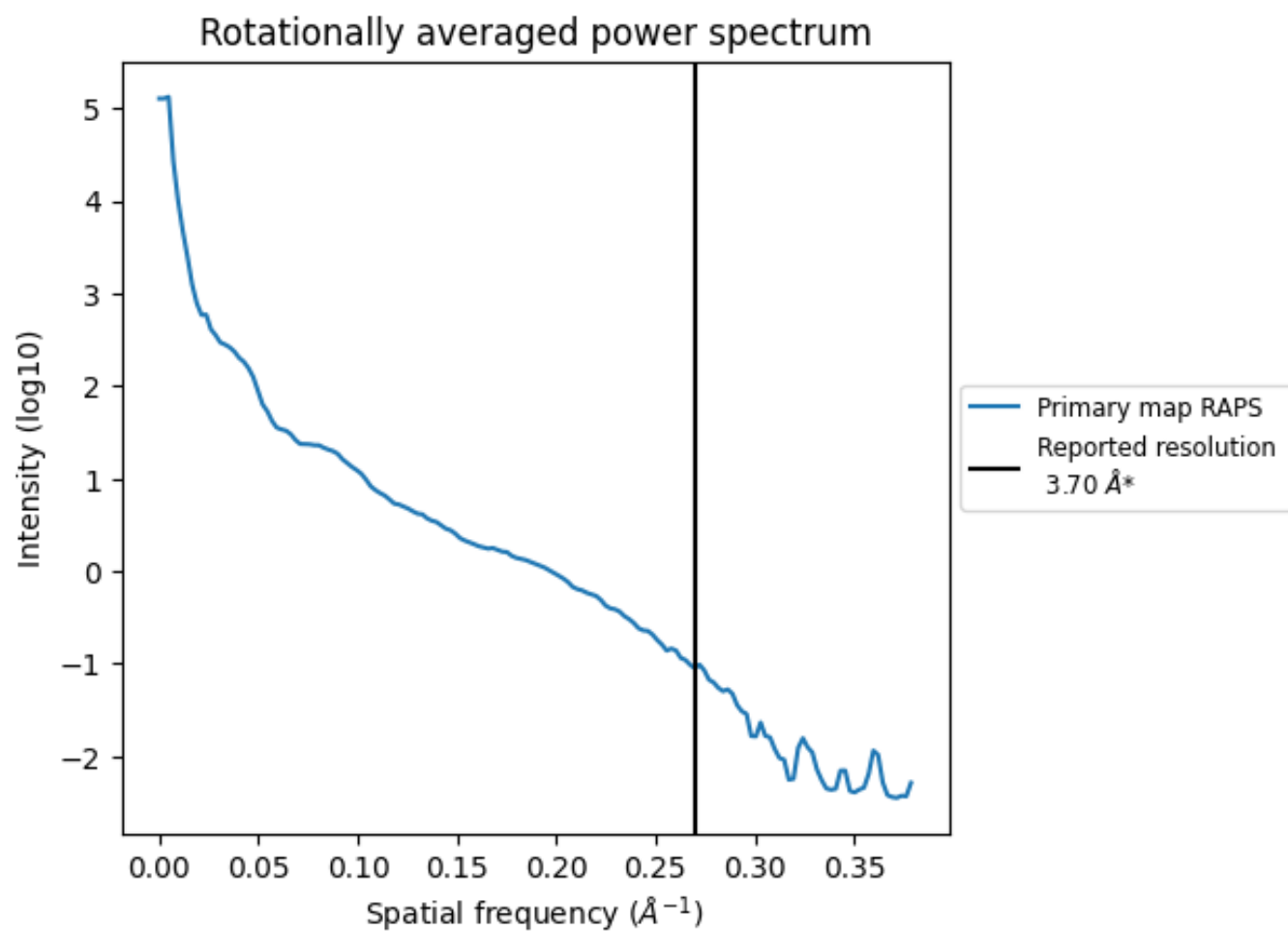
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2427 nm³; this corresponds to an approximate mass of 2193 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 ⓘ

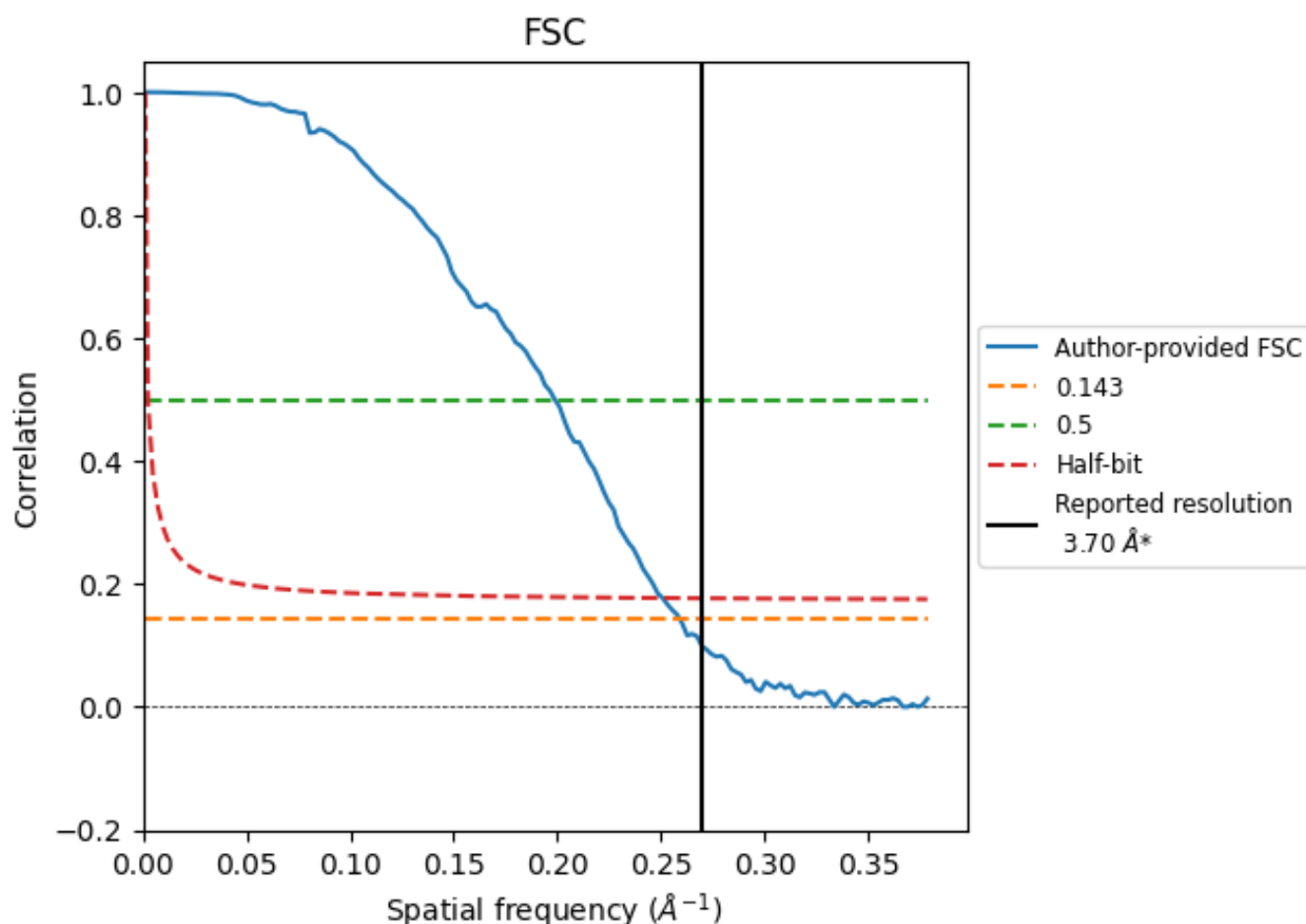


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

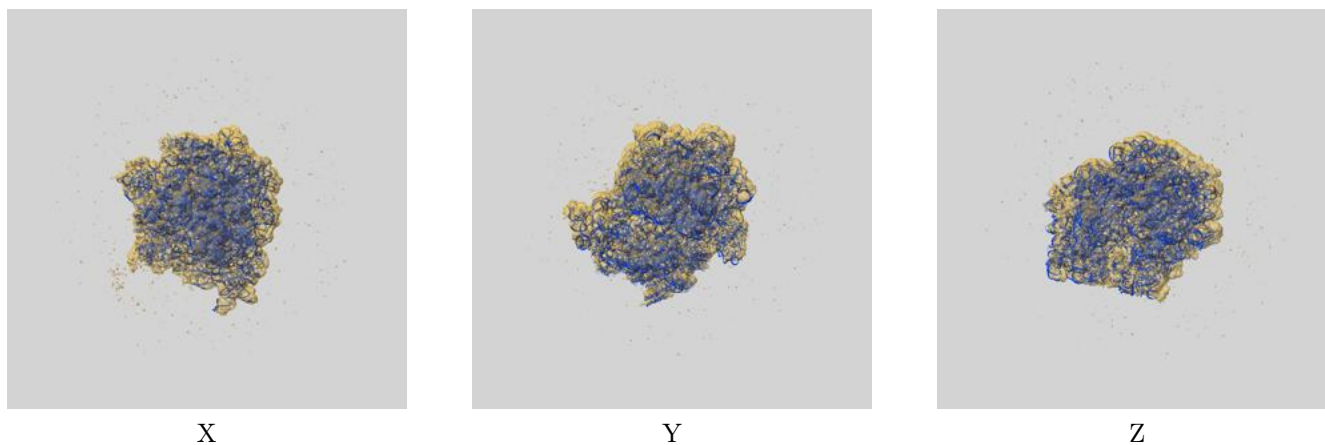
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.86	5.03	3.98
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

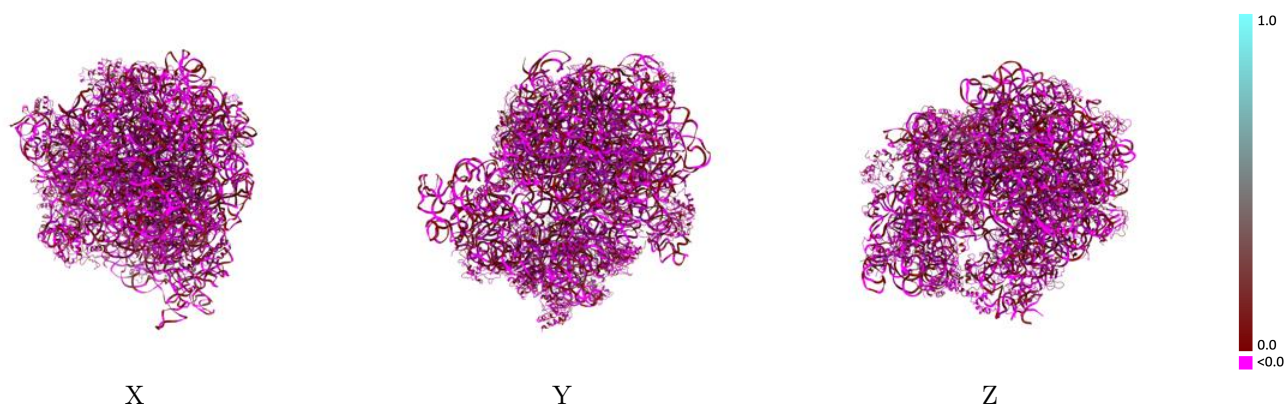
This section contains information regarding the fit between EMDB map EMD-6549 and PDB model 3JCD. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



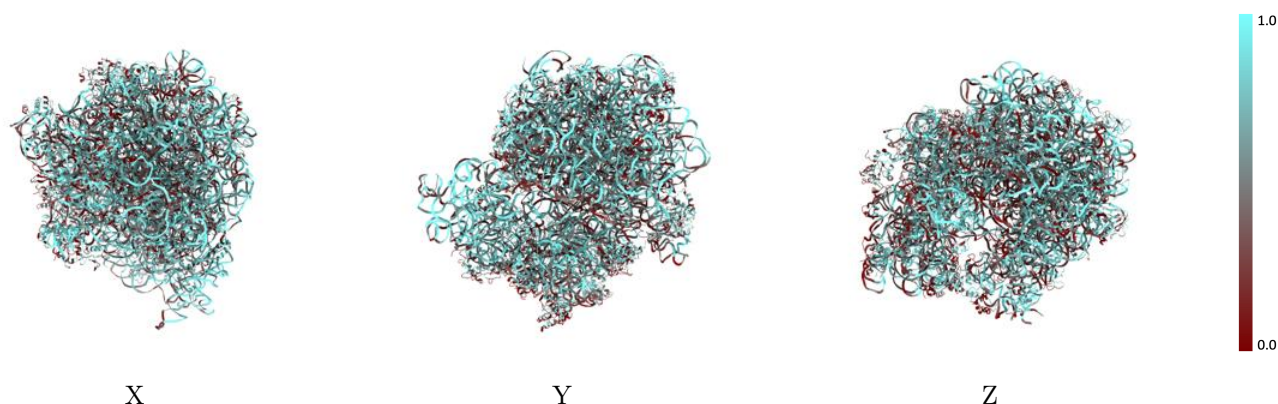
The images above show the 3D surface view of the map at the recommended contour level 0.0035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



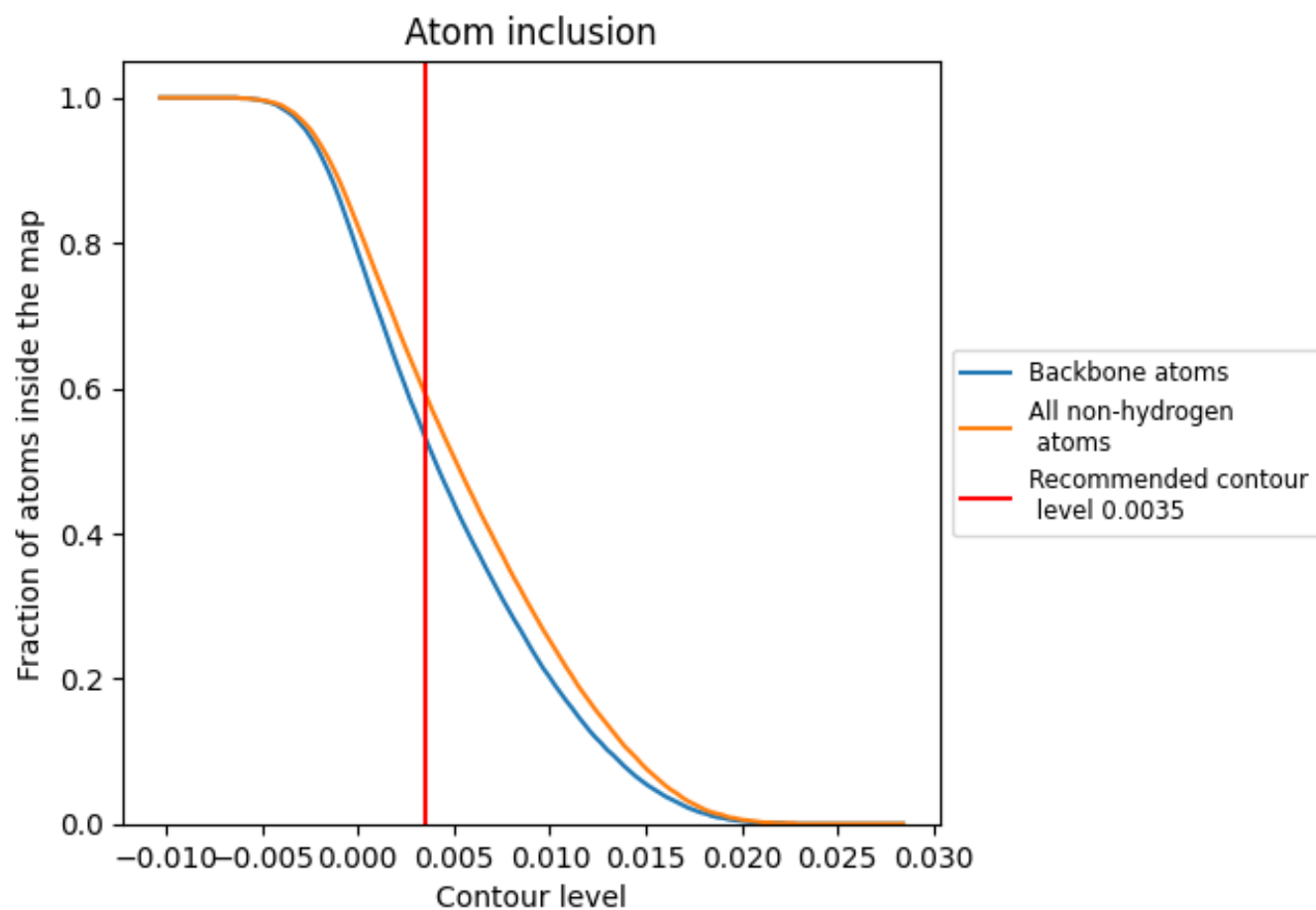
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 53% of all backbone atoms, 59% 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 (0.0035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5920	 -0.0090
0	 0.5490	 -0.0360
1	 0.3140	 -0.0230
2	 0.5100	 -0.0410
3	 0.6660	 -0.0270
4	 0.4790	 -0.0150
5	 0.6300	 0.0140
7	 0.4140	 -0.0520
8	 0.5510	 -0.0050
9	 0.5780	 0.0000
A	 0.6100	 -0.0110
B	 0.5990	 -0.0120
C	 0.4640	 0.0000
D	 0.5440	 -0.0090
E	 0.5630	 0.0040
F	 0.5040	 -0.0110
G	 0.5140	 -0.0030
H	 0.2990	 0.0010
I	 0.3980	 0.0020
J	 0.5480	 -0.0380
K	 0.4380	 0.0030
L	 0.6290	 0.0130
M	 0.3790	 -0.0370
N	 0.6090	 -0.0160
O	 0.6730	 0.0110
P	 0.4950	 -0.0160
Q	 0.6070	 -0.0210
R	 0.5910	 -0.0250
S	 0.5840	 -0.0010
T	 0.5720	 -0.0090
U	 0.6310	 0.0030
V	 0.4950	 0.0040
W	 0.6020	 -0.0170
X	 0.6040	 -0.0110
Y	 0.5490	 -0.0290



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Chain	Atom inclusion	Q-score
Z	 0.4940	 -0.0240
a	 0.6580	 -0.0050
b	 0.4560	 -0.0090
c	 0.4420	 -0.0260
d	 0.4670	 -0.0240
e	 0.4180	 -0.0140
f	 0.6020	 0.0060
g	 0.4870	 -0.0360
h	 0.5180	 0.0140
i	 0.5540	 -0.0090
j	 0.4800	 0.0130
k	 0.4820	 -0.0170
l	 0.6490	 -0.0000
m	 0.4540	 -0.0300
n	 0.4270	 -0.0300
o	 0.6380	 -0.0380
p	 0.6250	 0.0420
q	 0.5810	 -0.0220
r	 0.5480	 -0.0020
s	 0.6880	 -0.0120
t	 0.6260	 -0.0280
u	 0.4800	 0.0160
x	 0.0910	 -0.0350