wwPDB EM Validation Summary Report

Oct 13, 2024 – 04:58 pm BST

PDB ID	:	6GZX
EMDB ID	:	EMD-0104
Title	:	T. thermophilus hibernating 100S ribosome (ice)
Authors	:	Flygaard, R.K.; Jenner, L.B.
Deposited on	:	2018-07-05
Resolution	:	4.57 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

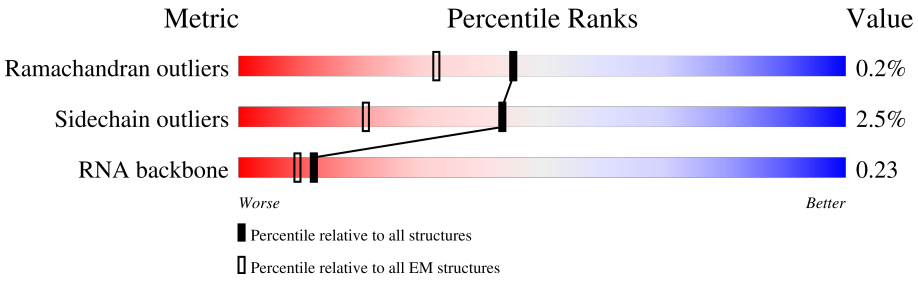
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	: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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.57 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	C1	272	50% 96% .
1	C2	272	46% 95% 5%
2	D1	205	40% 98% .
2	D2	205	38% 98% .
3	E1	208	37% 96% .
3	E2	208	32% 98% .
4	F1	181	30% 92% 8%
4	F2	181	32% 94% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	G1	170	25% 95% 5%
5	G2	170	27% 96%
6	H1	50	54% 98%
6	H2	50	60% 100%
7	I1	138	16% 96%
7	I2	138	21% 94% 6%
8	J1	122	30% 97%
8	J2	122	27% 97%
9	K1	150	26% 97%
9	K2	150	25% 98%
10	L1	141	26% 99%
10	L2	141	26% 99%
11	M1	117	28% 98%
11	M2	117	27% 95% 5%
12	N1	111	19% 96%
12	N2	111	14% 97%
13	O1	137	40% 93% 7%
13	O2	137	43% 95% 5%
14	P1	117	33% 95% 5%
14	P2	117	35% 96%
15	Q1	101	50% 98%
15	Q2	101	50% 95% 5%
16	R1	113	45% 96%
16	R2	113	43% 93% 7%
17	S1	92	24% 99%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
17	S2	92	29% 96%
18	T1	102	46% 94% 6%
18	T2	102	47% 96%
19	U1	179	55% 98%
19	U2	179	52% 96%
20	V1	77	31% 96%
20	V2	77	30% 96%
21	W1	97	34% 95% 5%
21	W2	97	36% 96%
22	X1	69	19% 97%
22	X2	69	14% 97%
23	Y1	59	56% 98%
23	Y2	59	47% 100%
24	Z1	63	17% 86% 11%
24	Z2	63	21% 94% 6%
25	a1	59	29% 100%
25	a2	59	32% 97%
26	b1	45	9% 89% 11%
26	b2	45	13% 89% 9%
27	c1	49	35% 94% 6%
27	c2	49	33% 98%
28	d1	61	49% 93% 7%
28	d2	61	46% 98%
29	A1	2912	5% 36% 51% 13%
29	A2	2912	5% 36% 50% 14%

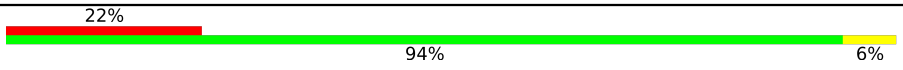
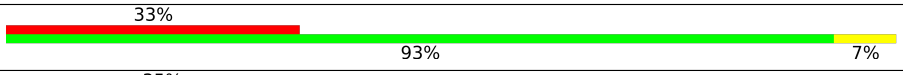
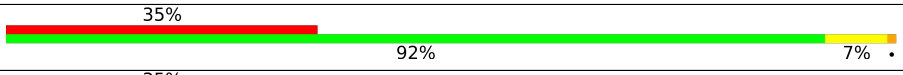
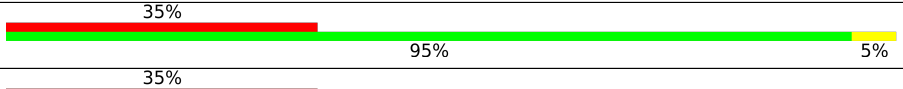
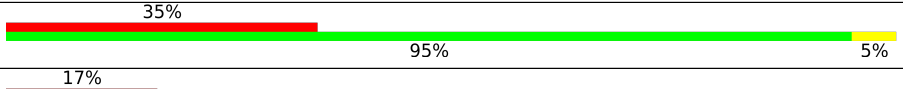
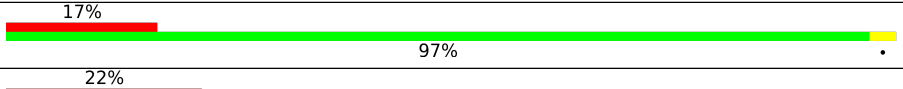
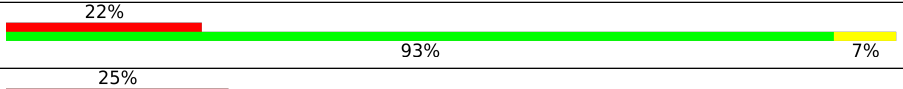
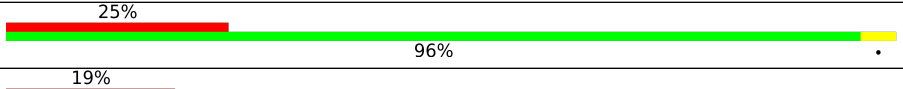
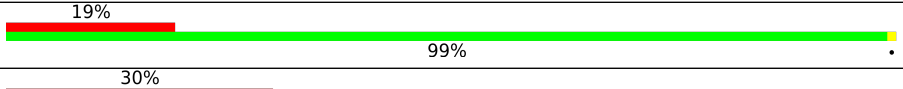
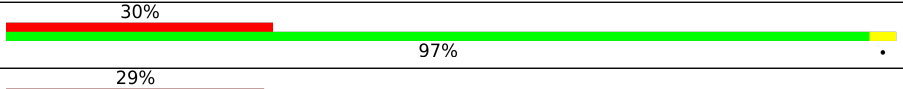
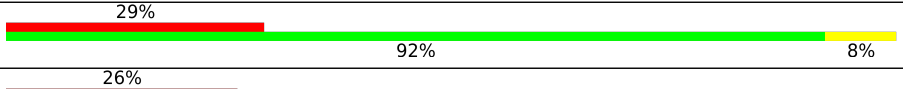
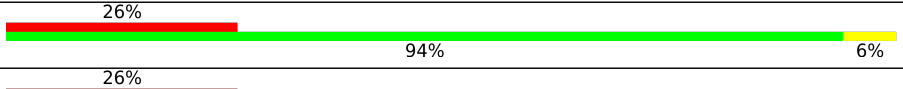
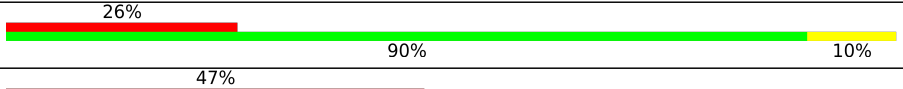
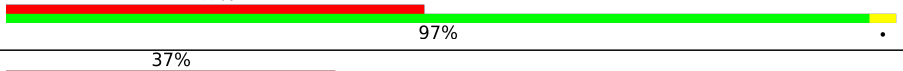
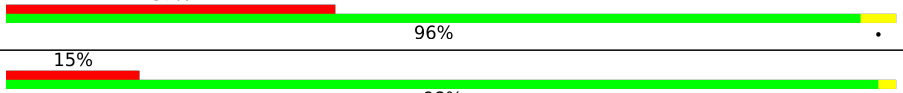
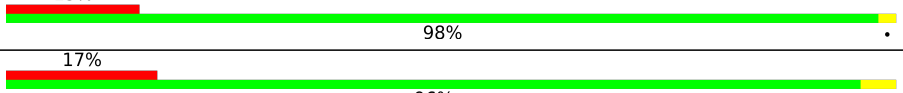
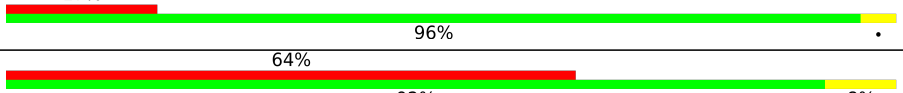
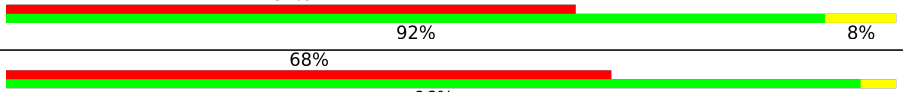
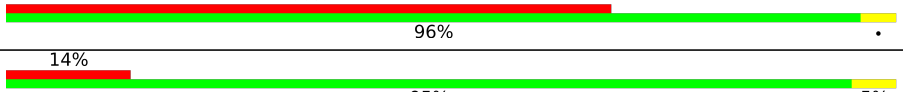
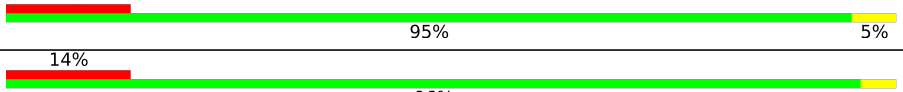
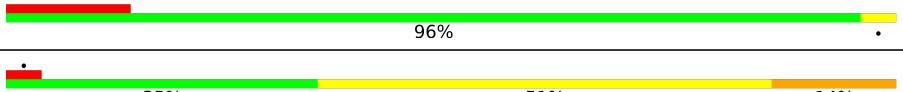
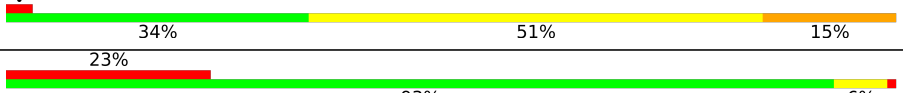
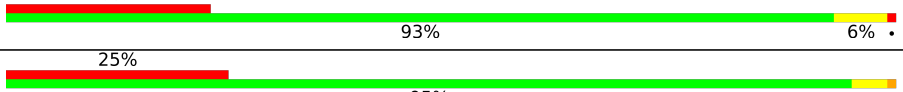
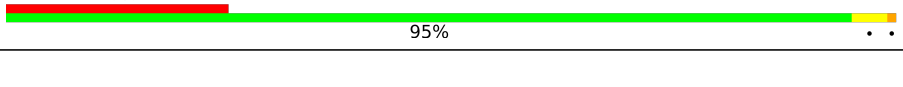
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
30	B1	122	42% 48% 11%
30	B2	122	43% 41% 16%
31	e1	36	17% 97%
31	e2	36	17% 97%
32	B3	237	30% 94% 6%
32	B4	237	30% 94% 6%
33	C3	206	33% 98%
33	C4	206	31% 98%
34	D3	208	15% 92% 8%
34	D4	208	15% 94% 6%
35	E3	151	23% 97%
35	E4	151	21% 98%
36	F3	101	36% 95% 5%
36	F4	101	38% 98%
37	G3	155	46% 95% 5%
37	G4	155	46% 97%
38	H3	138	20% 98%
38	H4	138	20% 94% 6%
39	I3	127	75% 94%
39	I4	127	72% 95% 5%
40	J3	99	61% 96%
40	J4	99	65% 95%
41	K3	118	36% 97%
41	K4	118	31% 98%
42	L3	125	20% 94% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
42	L4	125	
43	M3	117	
43	M4	117	
44	N3	60	
44	N4	60	
45	O3	88	
45	O4	88	
46	P3	84	
46	P4	84	
47	Q3	100	
47	Q4	100	
48	R3	62	
48	R4	62	
49	S3	78	
49	S4	78	
50	T3	99	
50	T4	99	
51	U3	25	
51	U4	25	
52	W4	57	
52	X3	57	
53	A3	1506	
53	A4	1506	
54	V3	119	
54	V4	119	

2 Entry composition (i)

There are 54 unique types of molecules in this entry. The entry contains 289188 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	C1	272	Total	C	N	O	S	0	0
			2116	1335	420	358	3		
1	C2	272	Total	C	N	O	S	0	0
			2116	1335	420	358	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D1	205	Total	C	N	O	S	0	0
			1569	991	300	272	6		
2	D2	205	Total	C	N	O	S	0	0
			1569	991	300	272	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E1	208	Total	C	N	O	S	0	0
			1628	1037	304	284	3		
3	E2	208	Total	C	N	O	S	0	0
			1628	1037	304	284	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F1	181	Total	C	N	O	S	0	0
			1474	942	268	260	4		
4	F2	181	Total	C	N	O	S	0	0
			1474	942	268	260	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G1	170	Total	C	N	O	S	0	0
			1308	829	245	233	1		
5	G2	170	Total	C	N	O	S	0	0
			1308	829	245	233	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H1	50	Total	C	N	O	S	0	0
			383	245	66	71	1		
6	H2	50	Total	C	N	O	S	0	0
			383	245	66	71	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I1	138	Total	C	N	O	S	0	0
			1105	712	206	183	4		
7	I2	138	Total	C	N	O	S	0	0
			1105	712	206	183	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J1	122	Total	C	N	O	S	0	0
			933	588	171	170	4		
8	J2	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K1	150	Total	C	N	O	S	0	0
			1145	712	232	198	3		
9	K2	150	Total	C	N	O	S	0	0
			1145	712	232	198	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L1	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L2	141	Total 1122	C 715	N 212	O 188	S 7	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
11	M1	117	Total 960	C 599	N 202	O 159	0	0
11	M2	117	Total 960	C 599	N 202	O 159	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
12	N1	111	Total 882	C 556	N 176	O 150	0	0
12	N2	111	Total 882	C 556	N 176	O 150	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O1	137	Total 1142	C 710	N 234	O 197	S 1	0	0
13	O2	137	Total 1142	C 710	N 234	O 197	S 1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P1	117	Total 964	C 610	N 202	O 151	S 1	0	0
14	P2	117	Total 964	C 610	N 202	O 151	S 1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q1	101	Total 779	C 501	N 142	O 135	S 1	0	0
15	Q2	101	Total 779	C 501	N 142	O 135	S 1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R1	113	Total	C	N	O	S	0	0
			900	566	177	155	2		
16	R2	113	Total	C	N	O	S	0	0
			900	566	177	155	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	S1	92	Total	C	N	O	0	0
			726	471	131	124		
17	S2	92	Total	C	N	O	0	0
			726	471	131	124		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T1	102	Total	C	N	O	S	0	0
			786	505	150	126	5		
18	T2	102	Total	C	N	O	S	0	0
			786	505	150	126	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U1	179	Total	C	N	O	S	0	0
			1429	911	255	260	3		
19	U2	179	Total	C	N	O	S	0	0
			1429	911	255	260	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V1	77	Total	C	N	O	S	0	0
			613	379	129	104	1		
20	V2	77	Total	C	N	O	S	0	0
			613	379	129	104	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W1	97	Total	C	N	O	S	0	0
			763	481	150	131	1		
21	W2	97	Total	C	N	O	S	0	0
			763	481	150	131	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X1	69	Total	C	N	O	S	0	0
			581	358	118	104	1		
22	X2	69	Total	C	N	O	S	0	0
			581	358	118	104	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
23	Y1	59	Total	C	N	O	0	0
			469	298	90	81		
23	Y2	59	Total	C	N	O	0	0
			469	298	90	81		

- Molecule 24 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z1	63	Total	C	N	O	S	0	0
			516	326	93	92	5		
24	Z2	63	Total	C	N	O	S	0	0
			516	326	93	92	5		

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a1	59	Total	C	N	O	S	0	0
			459	288	90	76	5		
25	a2	59	Total	C	N	O	S	0	0
			459	288	90	76	5		

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b1	45	Total	C	N	O	S	0	0
			390	241	79	66	4		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b2	45	Total	C	N	O	S	0	0
			390	241	79	66	4		

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c1	49	Total	C	N	O	S	0	0
			430	263	108	57	2		
27	c2	49	Total	C	N	O	S	0	0
			430	263	108	57	2		

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d1	61	Total	C	N	O	S	0	0
			489	312	99	76	2		
28	d2	61	Total	C	N	O	S	0	0
			489	312	99	76	2		

- Molecule 29 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A1	2912	Total	C	N	O	P	0	0
			62707	27911	11722	20163	2911		
29	A2	2912	Total	C	N	O	P	0	0
			62707	27911	11722	20163	2911		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A1	156	U	UNK	conflict	GB 55771382
A1	682	A	G	conflict	GB 55771382
A1	686	C	G	conflict	GB 55771382
A1	697	G	C	conflict	GB 55771382
A1	701	A	C	conflict	GB 55771382
A1	1106	U	G	conflict	GB 55771382
A1	1128	A	C	conflict	GB 55771382
A2	156	U	UNK	conflict	GB 55771382
A2	682	A	G	conflict	GB 55771382
A2	686	C	G	conflict	GB 55771382
A2	697	G	C	conflict	GB 55771382
A2	701	A	C	conflict	GB 55771382

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A2	1106	U	G	conflict	GB 55771382
A2	1128	A	C	conflict	GB 55771382

- Molecule 30 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B1	122	Total	C	N	O	P	0	0
			2617	1166	486	844	121		
30	B2	122	Total	C	N	O	P	0	0
			2617	1166	486	844	121		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e1	36	Total	C	N	O	S	0	0
			299	183	67	46	3		
31	e2	36	Total	C	N	O	S	0	0
			299	183	67	46	3		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B3	237	Total	C	N	O	S	0	0
			1925	1228	344	348	5		
32	B4	237	Total	C	N	O	S	0	0
			1925	1228	344	348	5		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C3	206	Total	C	N	O	S	0	0
			1613	1016	314	282	1		
33	C4	206	Total	C	N	O	S	0	0
			1613	1016	314	282	1		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	D3	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		
34	D4	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	E3	151	Total	C	N	O	S	0	0
			1156	729	218	205	4		
35	E4	151	Total	C	N	O	S	0	0
			1156	729	218	205	4		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	F3	101	Total	C	N	O	S	0	0
			843	531	155	154	3		
36	F4	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G3	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		
37	G4	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H3	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		
38	H4	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	I3	127	Total	C	N	O	0	0
			1010	639	197	174		
39	I4	127	Total	C	N	O	0	0
			1010	639	197	174		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J3	99	Total	C	N	O	S	0	0
			802	504	157	140	1		
40	J4	99	Total	C	N	O	S	0	0
			802	504	157	140	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K3	118	Total	C	N	O	S	0	0
			879	546	167	163	3		
41	K4	118	Total	C	N	O	S	0	0
			879	546	167	163	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L3	125	Total	C	N	O	S	0	0
			976	614	196	165	1		
42	L4	125	Total	C	N	O	S	0	0
			976	614	196	165	1		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M3	117	Total	C	N	O	S	0	0
			934	577	192	163	2		
43	M4	117	Total	C	N	O	S	0	0
			934	577	192	163	2		

- Molecule 44 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	N3	60	Total	C	N	O	S	0	0
			492	312	104	72	4		
44	N4	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	O3	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
45	O4	88	Total 734	C 459	N 147	O 126	S 2	0	0

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	P3	84	Total 706	C 446	N 140	O 119	S 1	0	0
46	P4	84	Total 706	C 446	N 140	O 119	S 1	0	0

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q3	100	Total 835	C 534	N 155	O 144	S 2	0	0
47	Q4	100	Total 835	C 534	N 155	O 144	S 2	0	0

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	R3	62	Total 515	C 328	N 101	O 86	0	0
48	R4	62	Total 515	C 328	N 101	O 86	0	0

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S3	78	Total 625	C 398	N 115	O 110	S 2	0	0
49	S4	78	Total 625	C 398	N 115	O 110	S 2	0	0

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	T3	99	Total 763	C 470	N 162	O 129	S 2	0	0
50	T4	99	Total 763	C 470	N 162	O 129	S 2	0	0

- Molecule 51 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	U3	25	Total	C	N	O	0	0
			218	134	52	32		
51	U4	25	Total	C	N	O	0	0
			218	134	52	32		

- Molecule 52 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	X3	57	Total	C	N	O	S	0	0
			476	304	85	84	3		
52	W4	57	Total	C	N	O	S	0	0
			476	304	85	84	3		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A3	1506	Total	C	N	O	P	0	0
			32369	14408	5997	10459	1505		
53	A4	1506	Total	C	N	O	P	0	0
			32369	14408	5997	10459	1505		

- Molecule 54 is a protein called Ribosome hibernation promoting factor.

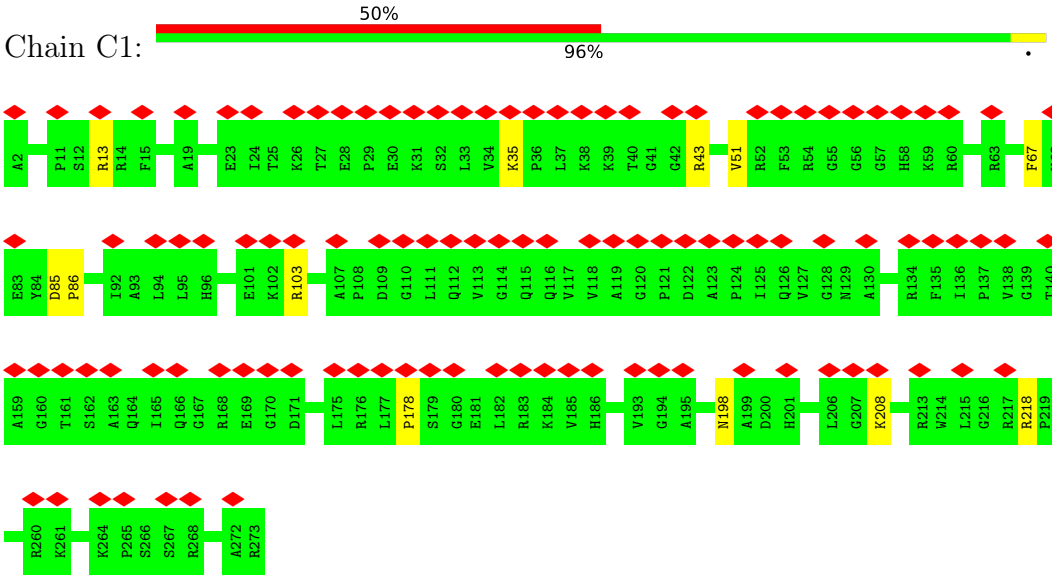
Mol	Chain	Residues	Atoms					AltConf	Trace
54	V3	119	Total	C	N	O	S	0	0
			963	603	179	180	1		
54	V4	119	Total	C	N	O	S	0	0
			963	603	179	180	1		

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.

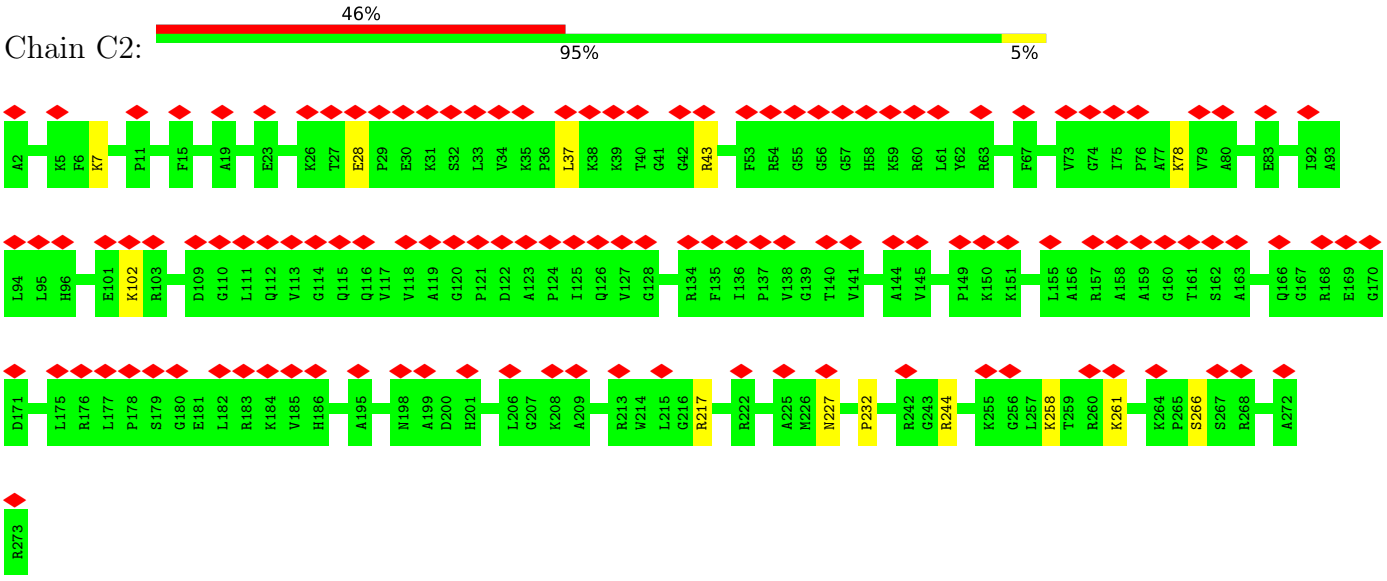
• Molecule 1: 50S ribosomal protein L2

Chain C1:



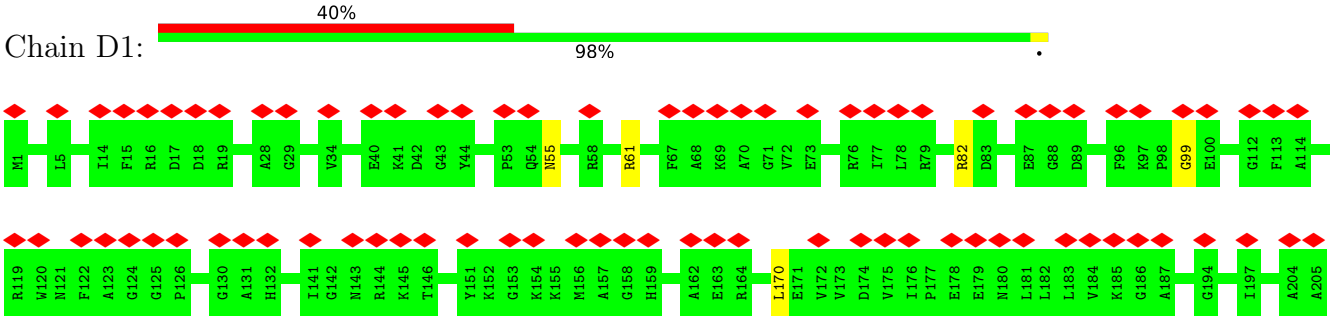
• Molecule 1: 50S ribosomal protein L2

Chain C2:



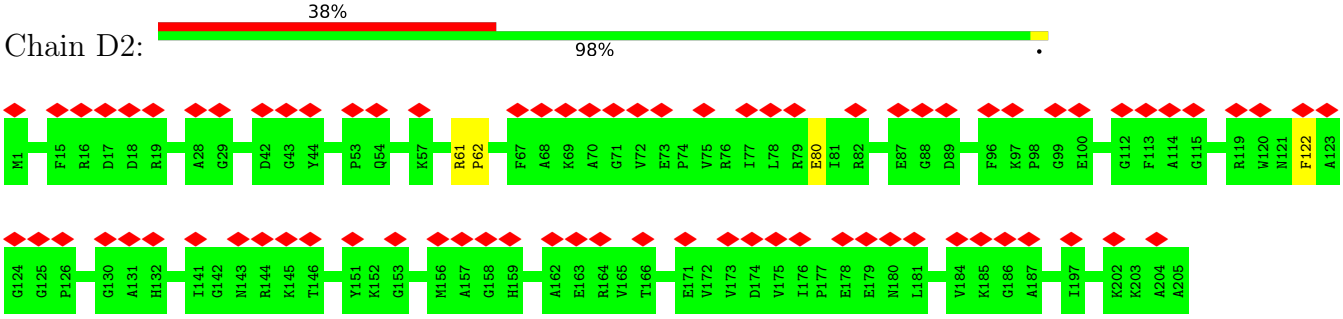
• Molecule 2: 50S ribosomal protein L3

Chain D1:



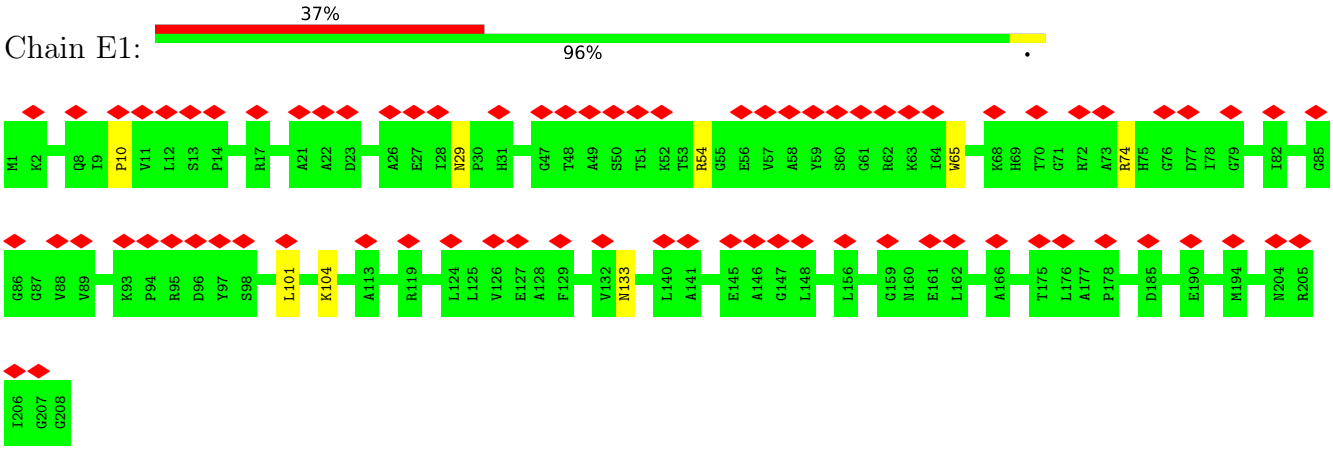
• Molecule 2: 50S ribosomal protein L3

Chain D2:



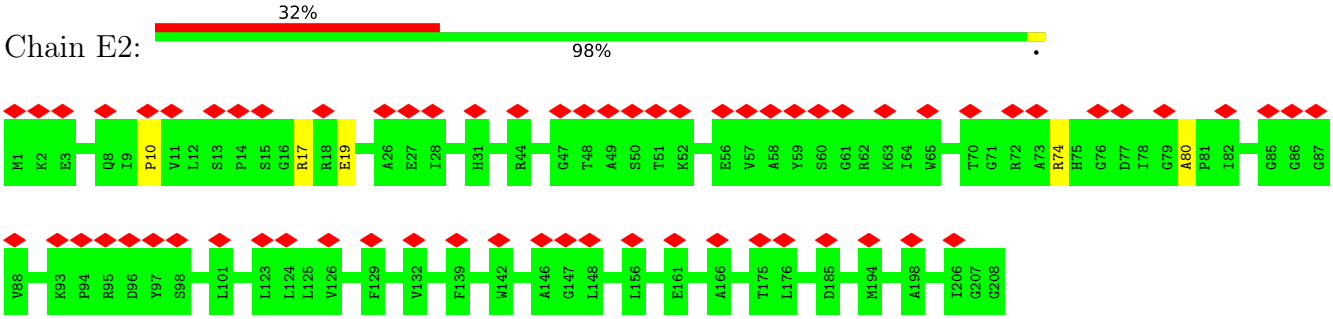
• Molecule 3: 50S ribosomal protein L4

Chain E1:



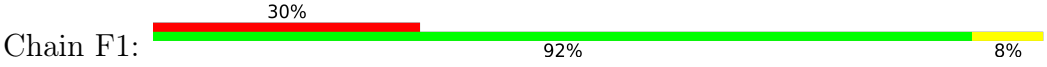
• Molecule 3: 50S ribosomal protein L4

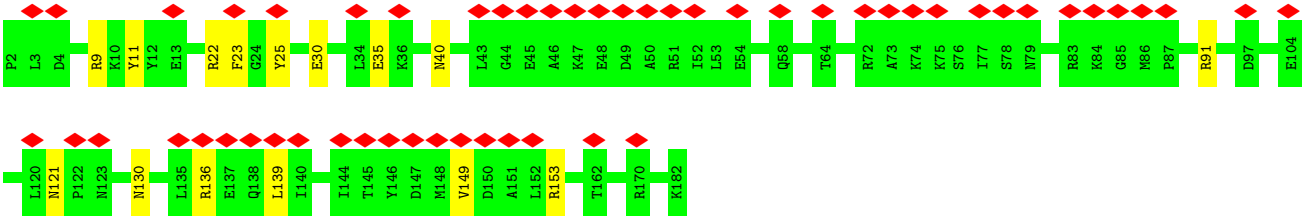
Chain E2:



• Molecule 4: 50S ribosomal protein L5

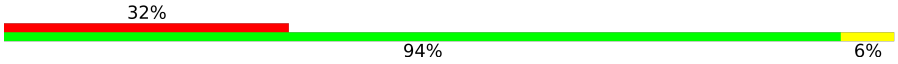
Chain F1:

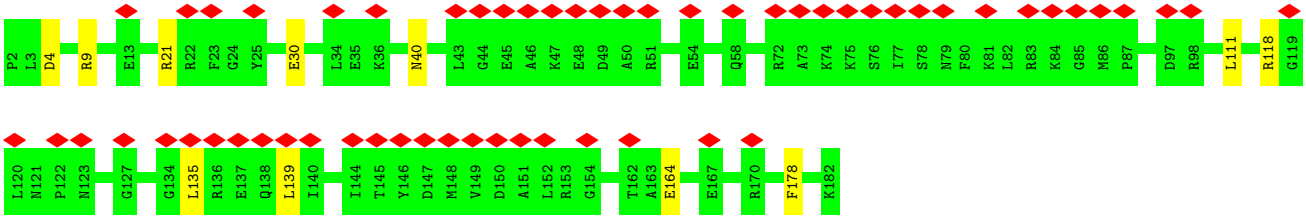




• Molecule 4: 50S ribosomal protein L5

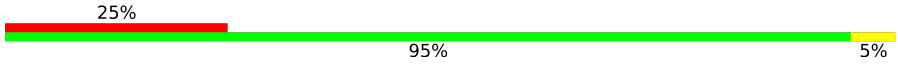
Chain F2:

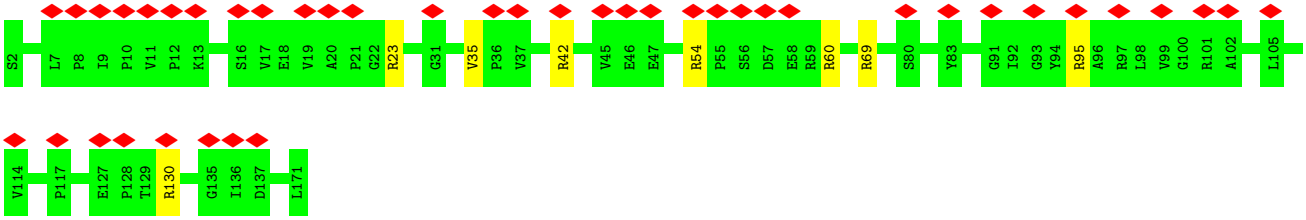




• Molecule 5: 50S ribosomal protein L6

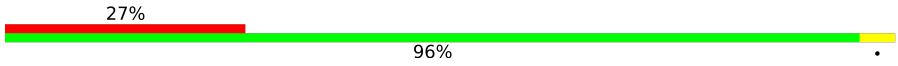
Chain G1:

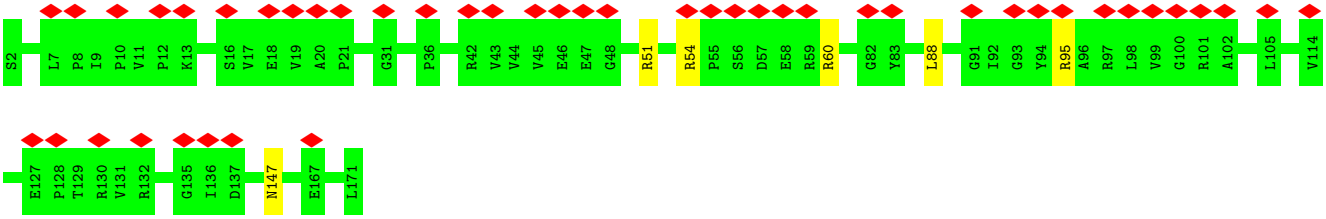




• Molecule 5: 50S ribosomal protein L6

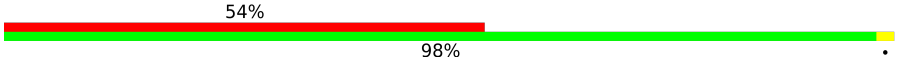
Chain G2:

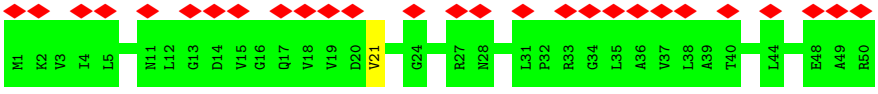




• Molecule 6: 50S ribosomal protein L9

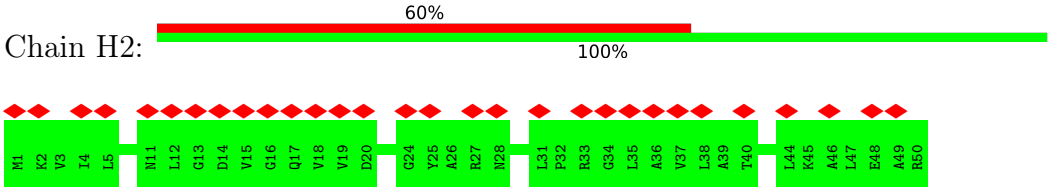
Chain H1:





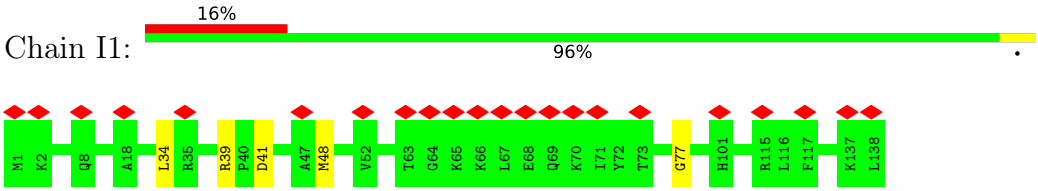
• Molecule 6: 50S ribosomal protein L9

Chain H2:



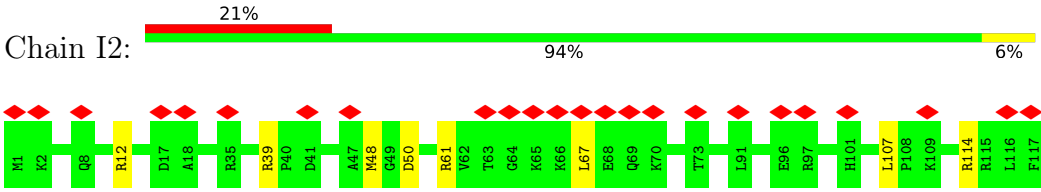
• Molecule 7: 50S ribosomal protein L13

Chain I1:



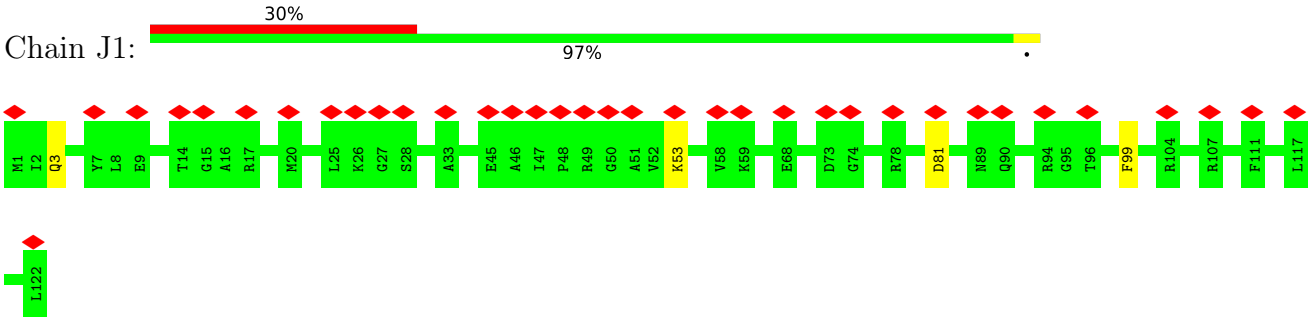
• Molecule 7: 50S ribosomal protein L13

Chain I2:



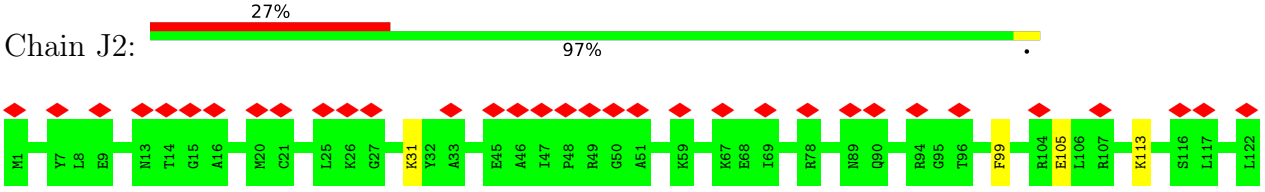
• Molecule 8: 50S ribosomal protein L14

Chain J1:



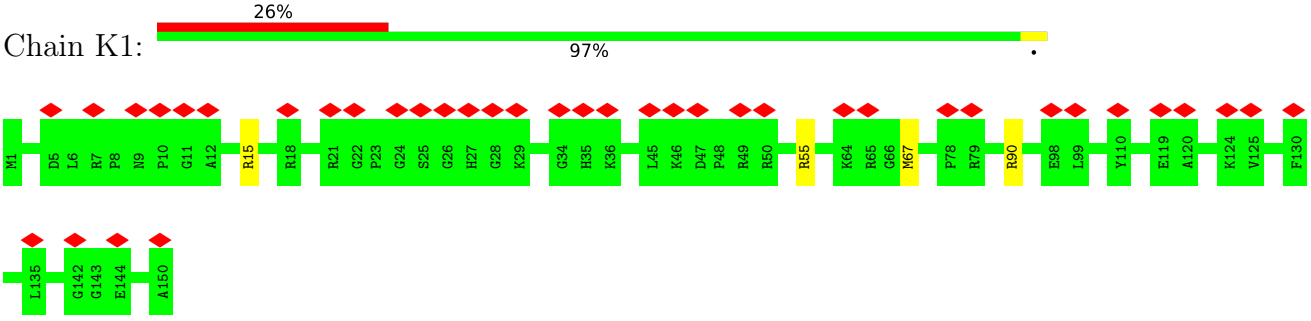
• Molecule 8: 50S ribosomal protein L14

Chain J2:



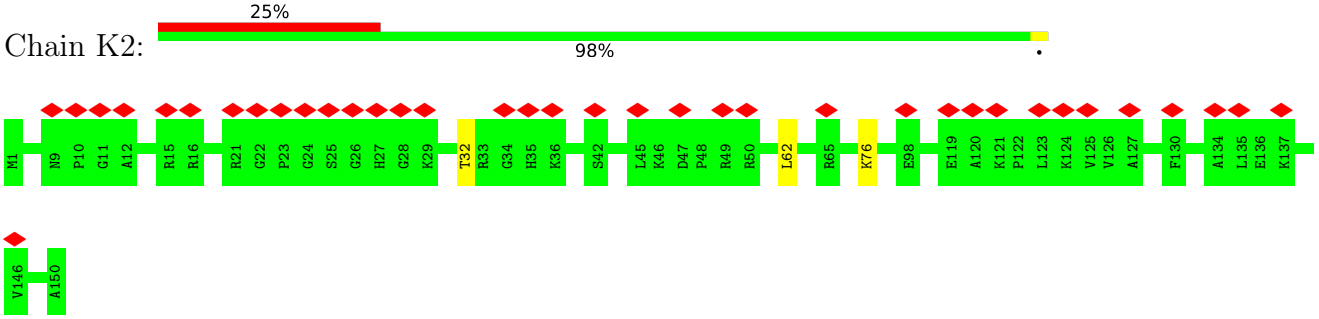
• Molecule 9: 50S ribosomal protein L15

Chain K1:



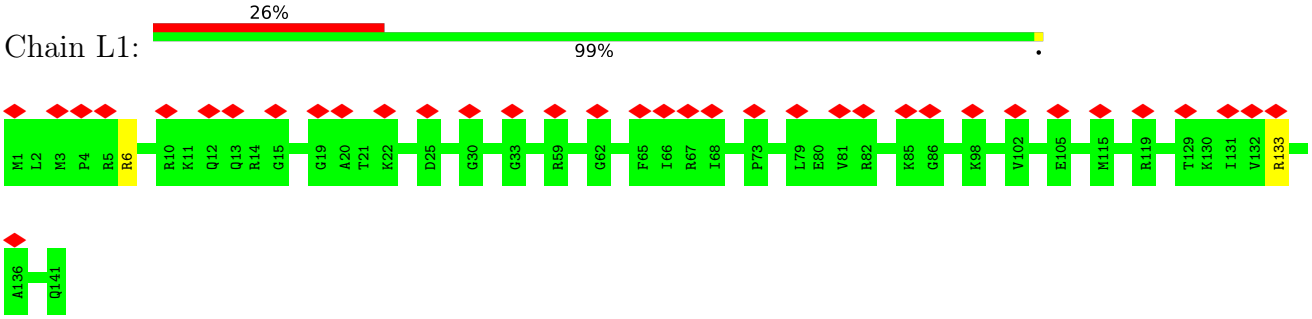
• Molecule 9: 50S ribosomal protein L15

Chain K2:



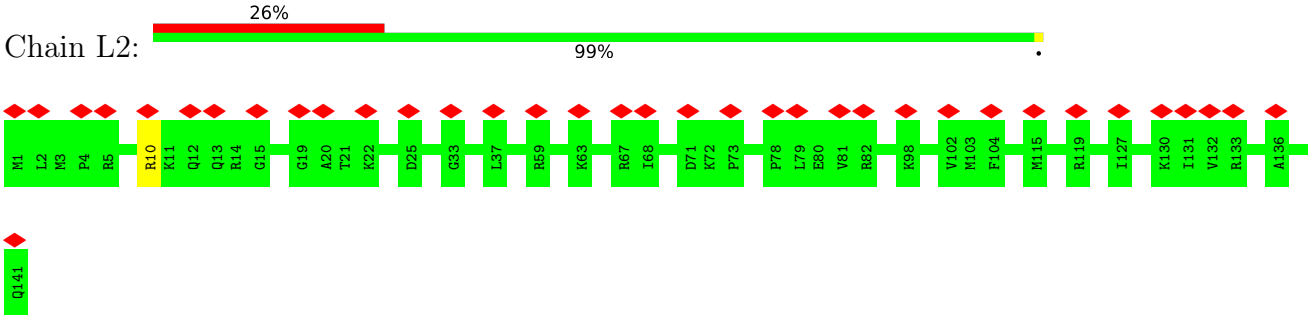
• Molecule 10: 50S ribosomal protein L16

Chain L1:



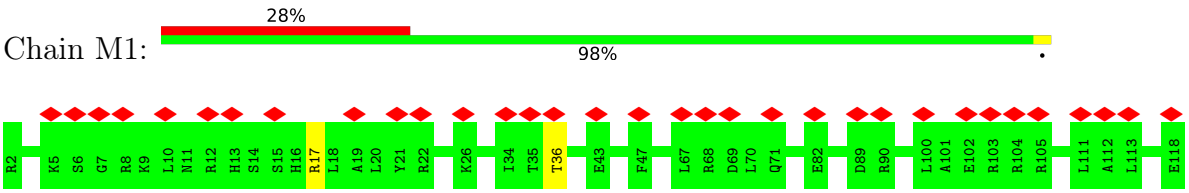
• Molecule 10: 50S ribosomal protein L16

Chain L2:



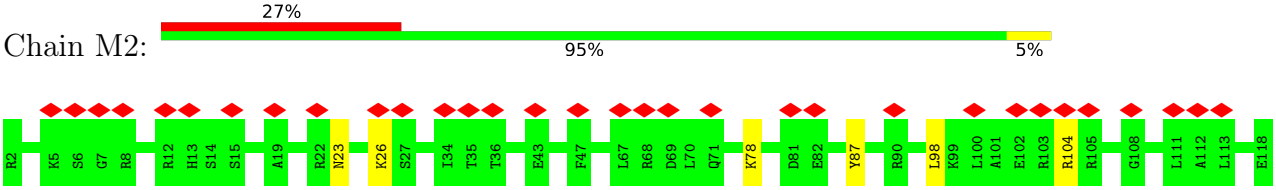
• Molecule 11: 50S ribosomal protein L17

Chain M1:



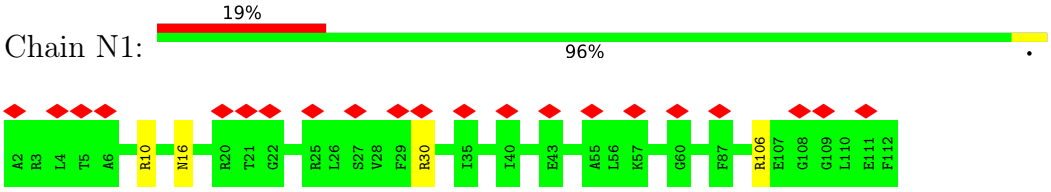
• Molecule 11: 50S ribosomal protein L17

Chain M2:



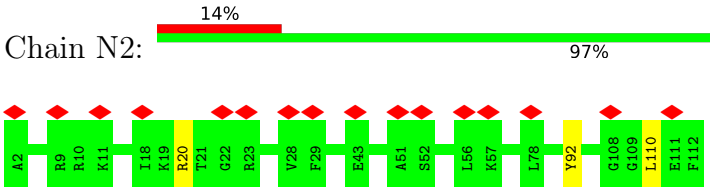
• Molecule 12: 50S ribosomal protein L18

Chain N1:



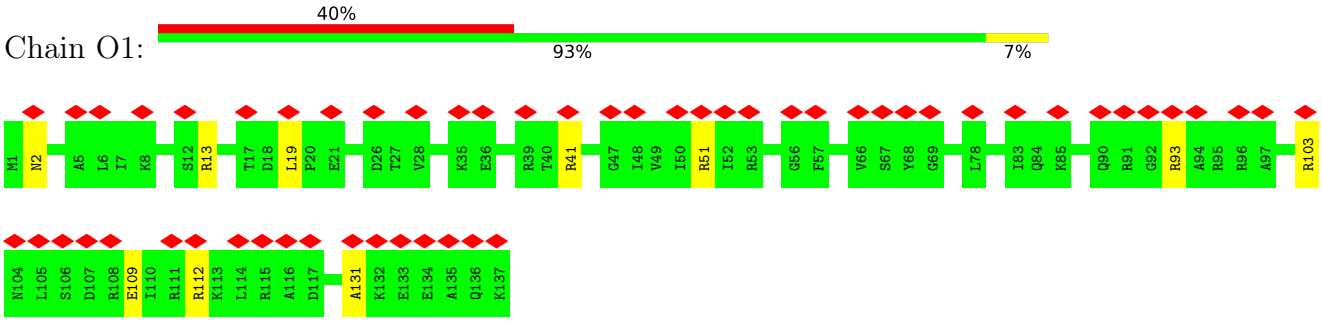
• Molecule 12: 50S ribosomal protein L18

Chain N2:



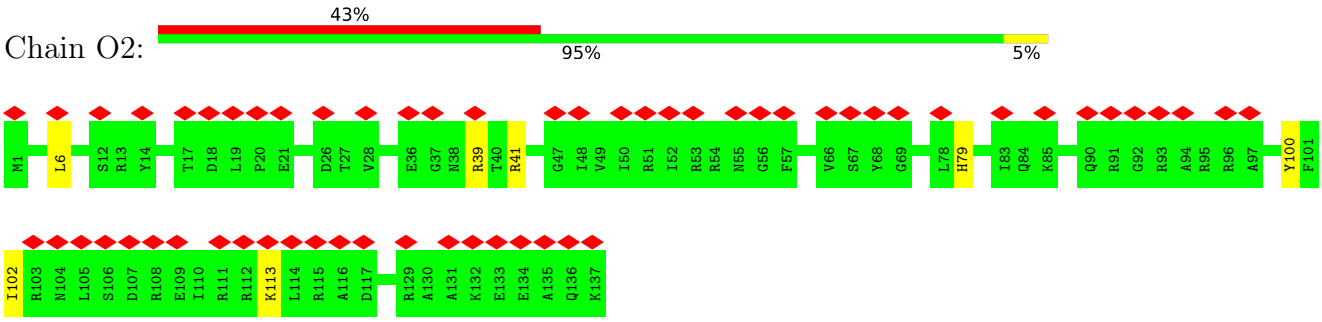
• Molecule 13: 50S ribosomal protein L19

Chain O1:



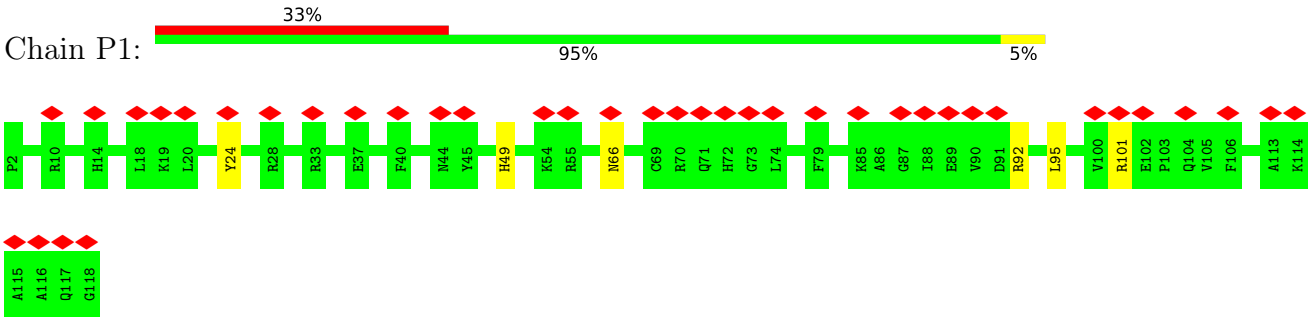
• Molecule 13: 50S ribosomal protein L19

Chain O2:



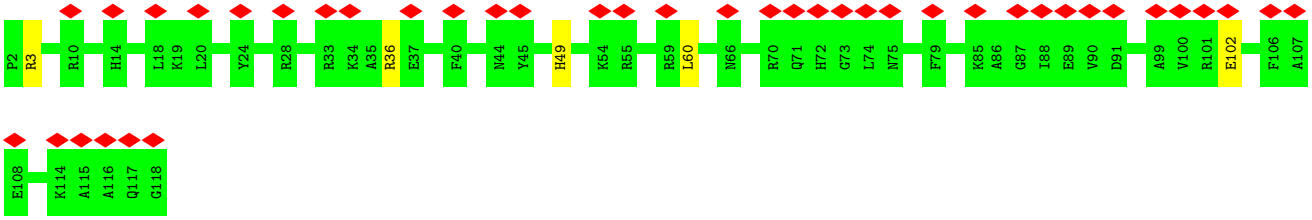
• Molecule 14: 50S ribosomal protein L20

Chain P1:



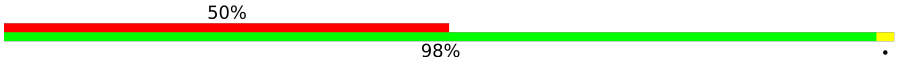
• Molecule 14: 50S ribosomal protein L20

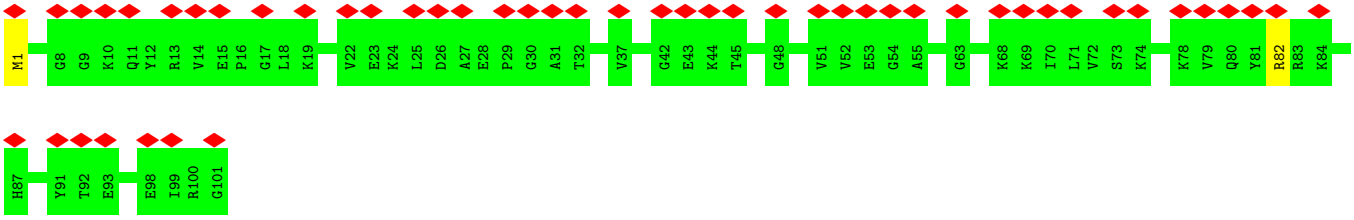
Chain P2:



• Molecule 15: 50S ribosomal protein L21

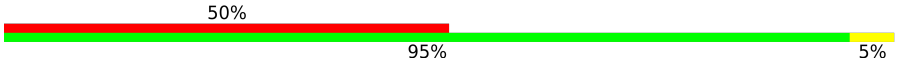
Chain Q1:

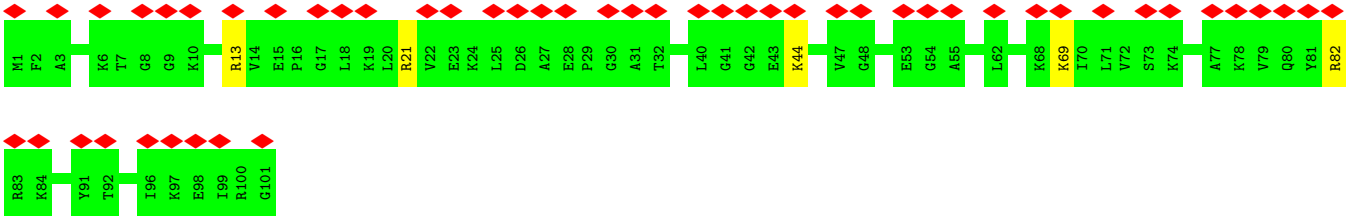




• Molecule 15: 50S ribosomal protein L21

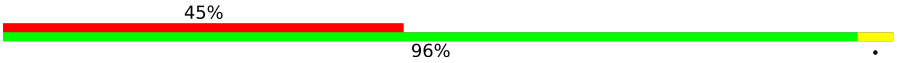
Chain Q2:

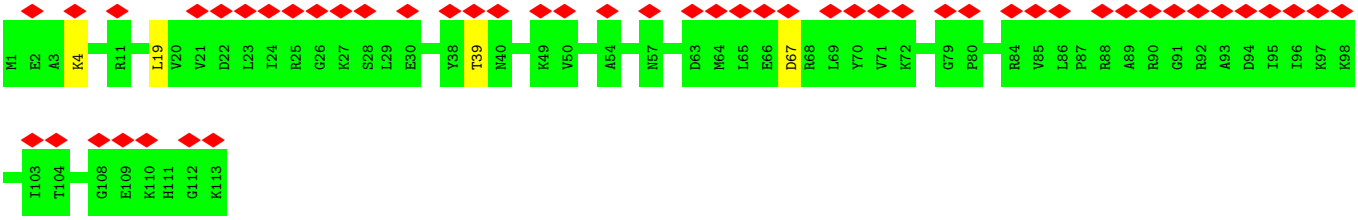




• Molecule 16: 50S ribosomal protein L22

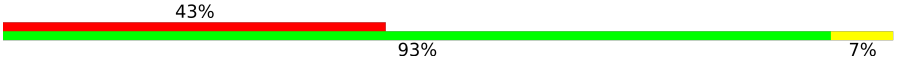
Chain R1:

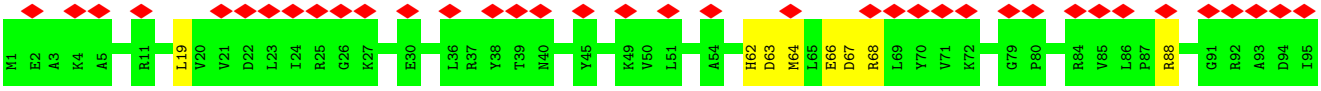


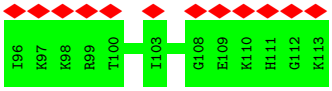


• Molecule 16: 50S ribosomal protein L22

Chain R2:

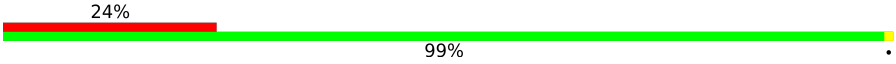


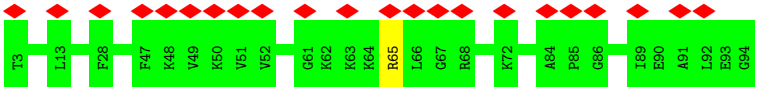




• Molecule 17: 50S ribosomal protein L23

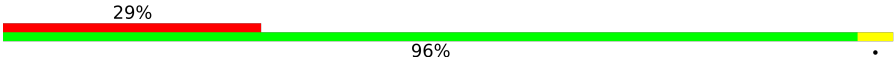
Chain S1:

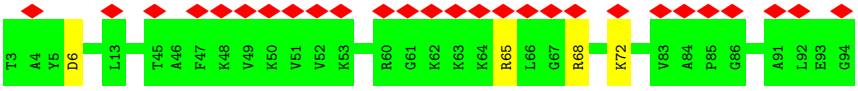




• Molecule 17: 50S ribosomal protein L23

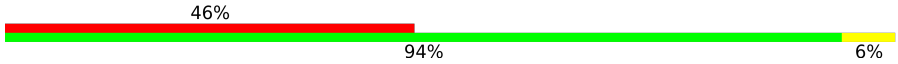
Chain S2:

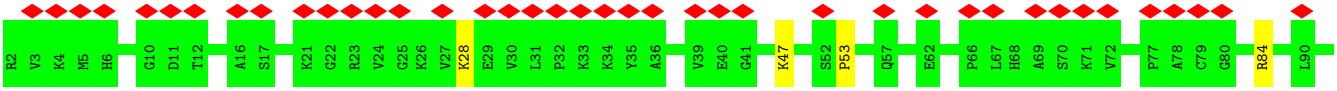


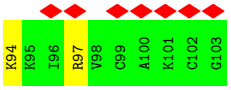


• Molecule 18: 50S ribosomal protein L24

Chain T1:

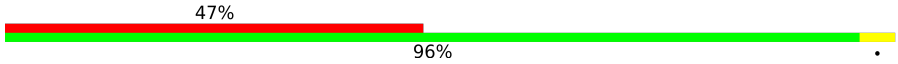


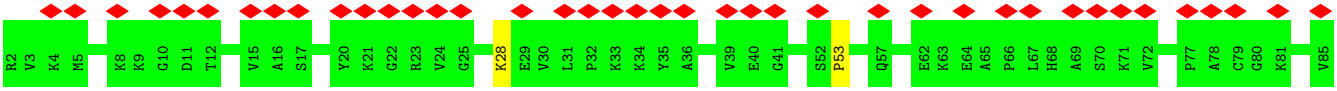


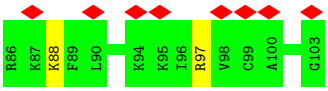


• Molecule 18: 50S ribosomal protein L24

Chain T2:

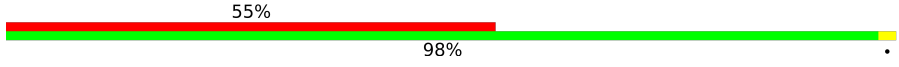


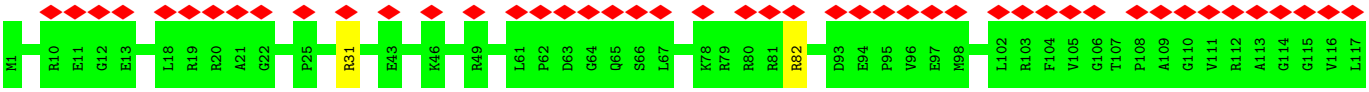


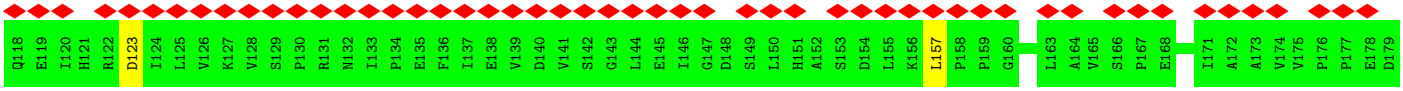


• Molecule 19: 50S ribosomal protein L25

Chain U1:

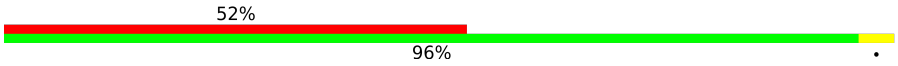


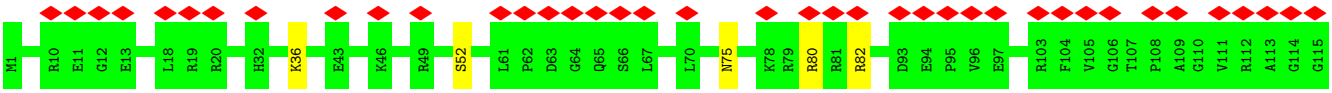


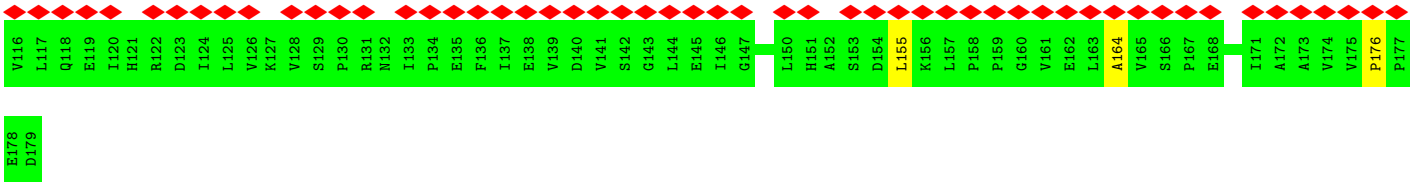


• Molecule 19: 50S ribosomal protein L25

Chain U2:

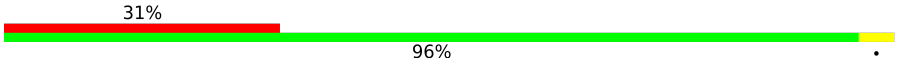


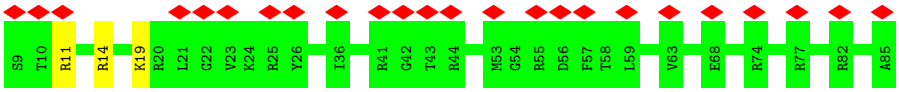




• Molecule 20: 50S ribosomal protein L27

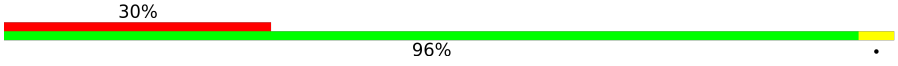
Chain V1:

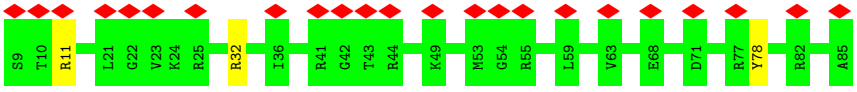




• Molecule 20: 50S ribosomal protein L27

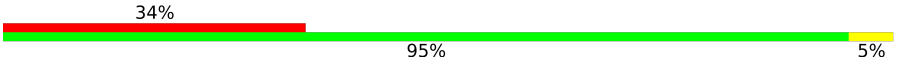
Chain V2:

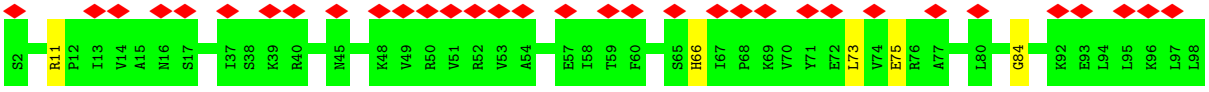




• Molecule 21: 50S ribosomal protein L28

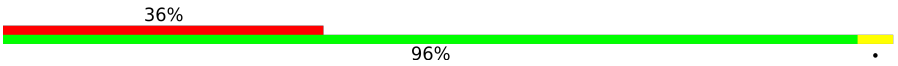
Chain W1:

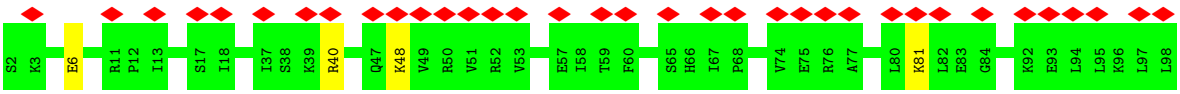




• Molecule 21: 50S ribosomal protein L28

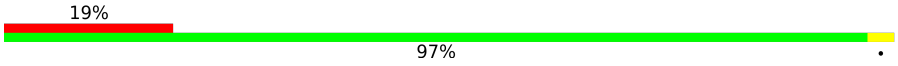
Chain W2:

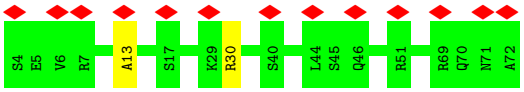




• Molecule 22: 50S ribosomal protein L29

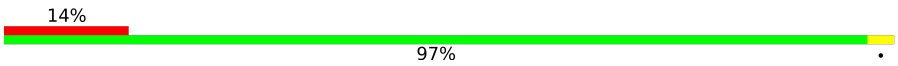
Chain X1:

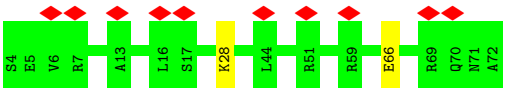




• Molecule 22: 50S ribosomal protein L29

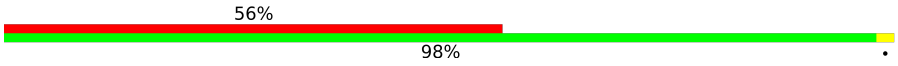
Chain X2:

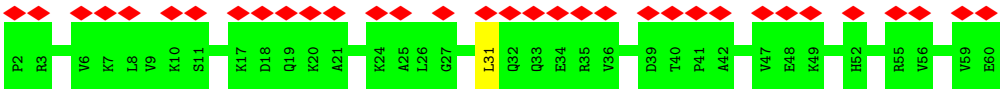




• Molecule 23: 50S ribosomal protein L30

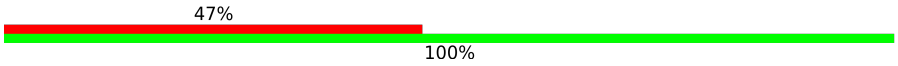
Chain Y1:

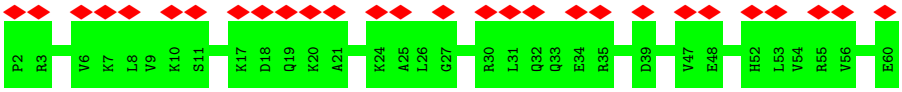




• Molecule 23: 50S ribosomal protein L30

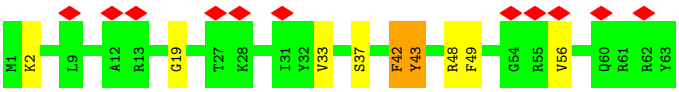
Chain Y2:





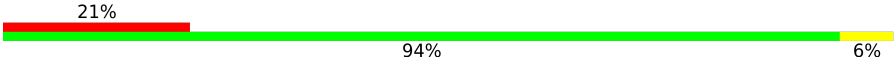
• Molecule 24: 50S ribosomal protein L31

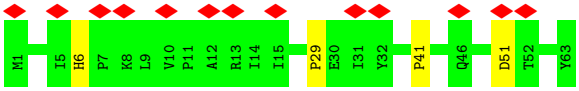
Chain Z1:



• Molecule 24: 50S ribosomal protein L31

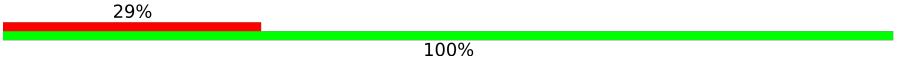
Chain Z2:

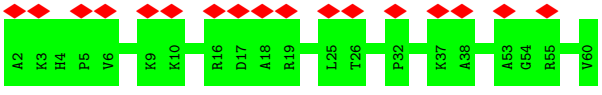




• Molecule 25: 50S ribosomal protein L32

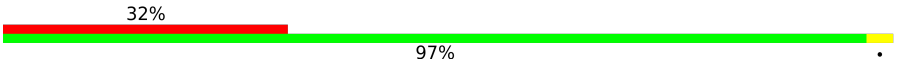
Chain a1:

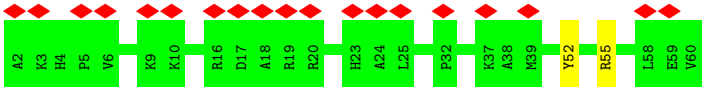




• Molecule 25: 50S ribosomal protein L32

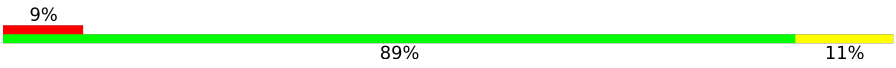
Chain a2:

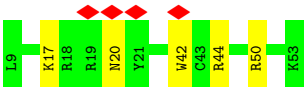




• Molecule 26: 50S ribosomal protein L33

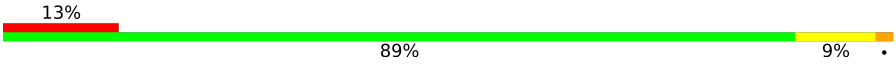
Chain b1:

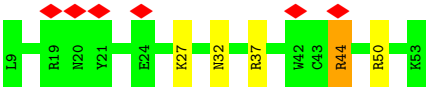




• Molecule 26: 50S ribosomal protein L33

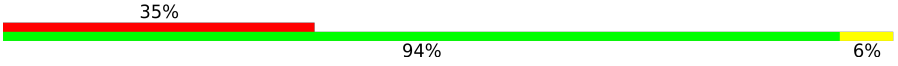
Chain b2:

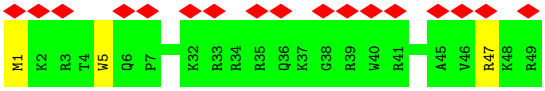




• Molecule 27: 50S ribosomal protein L34

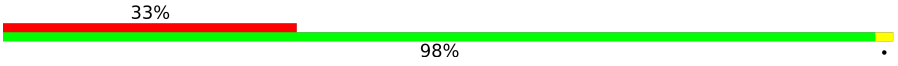
Chain c1:

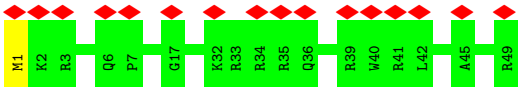




• Molecule 27: 50S ribosomal protein L34

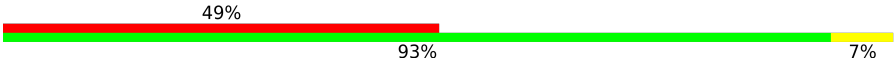
Chain c2:

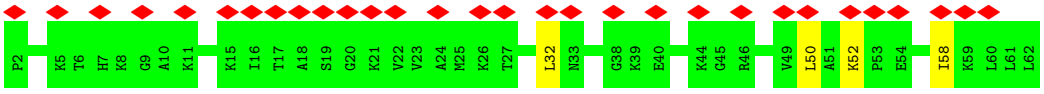




• Molecule 28: 50S ribosomal protein L35

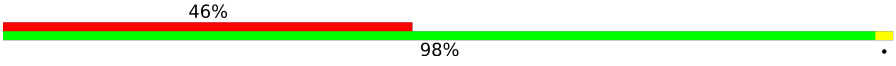
Chain d1:

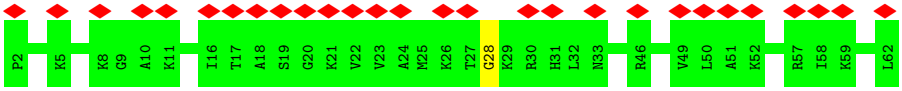




• Molecule 28: 50S ribosomal protein L35

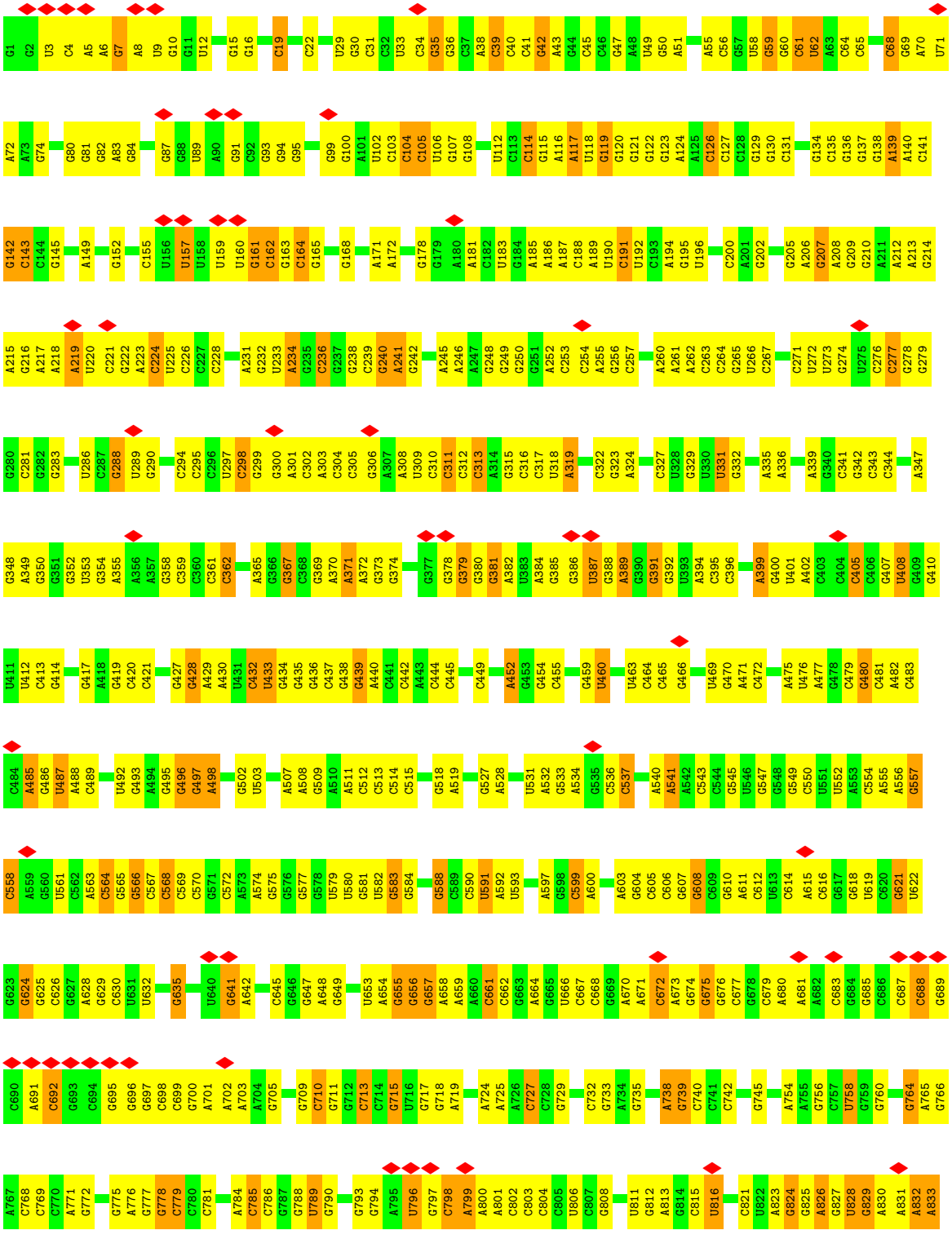
Chain d2:

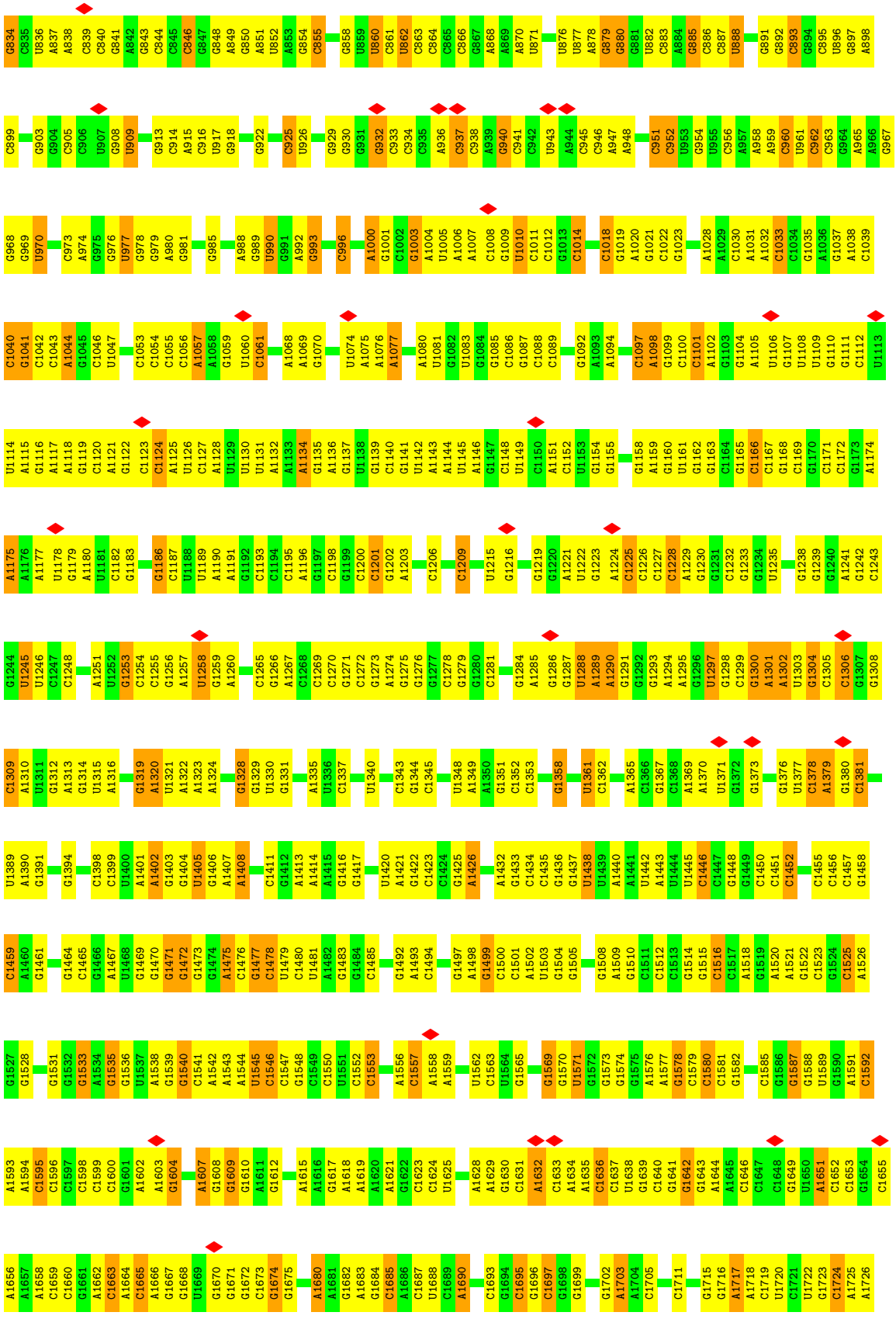


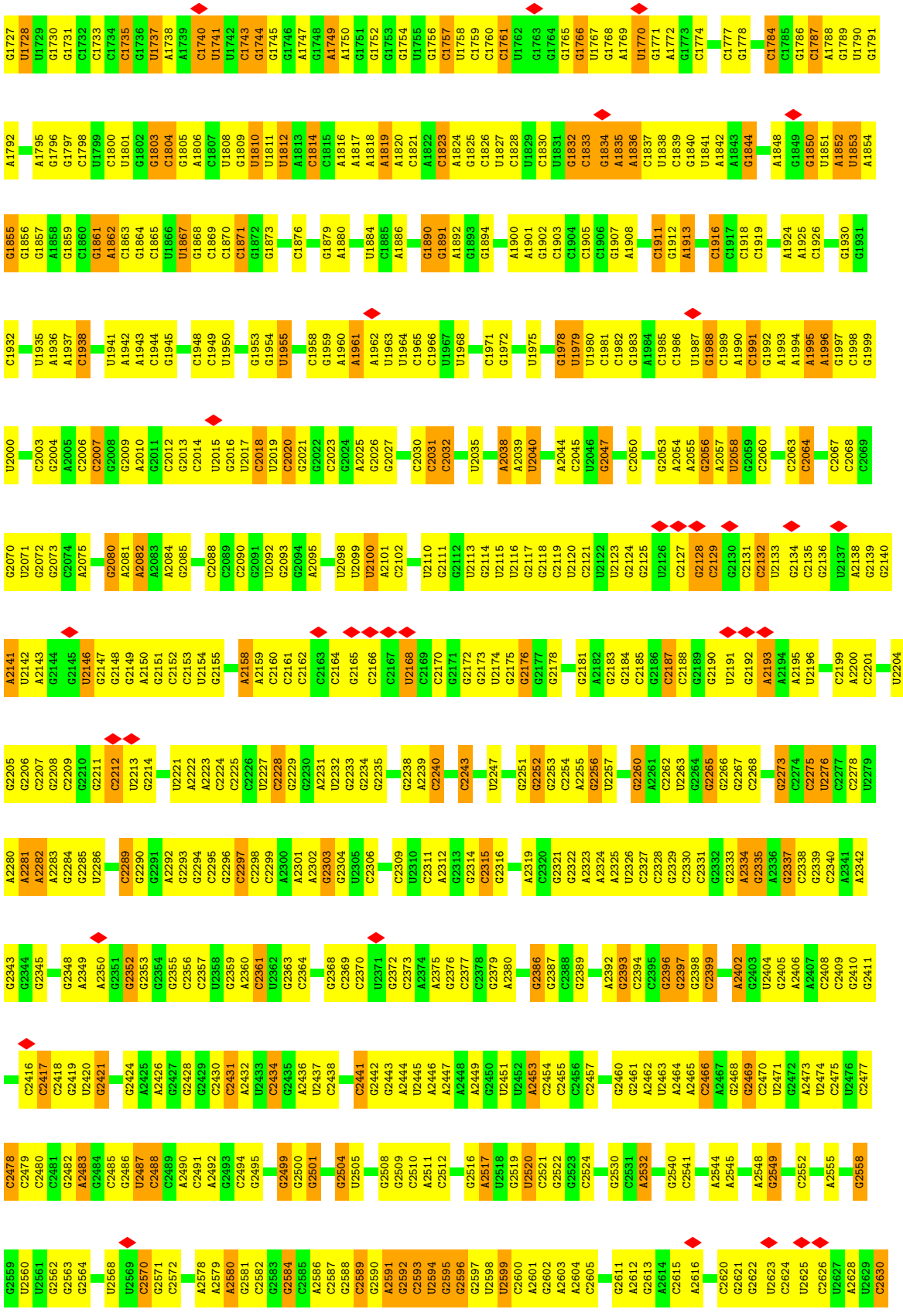


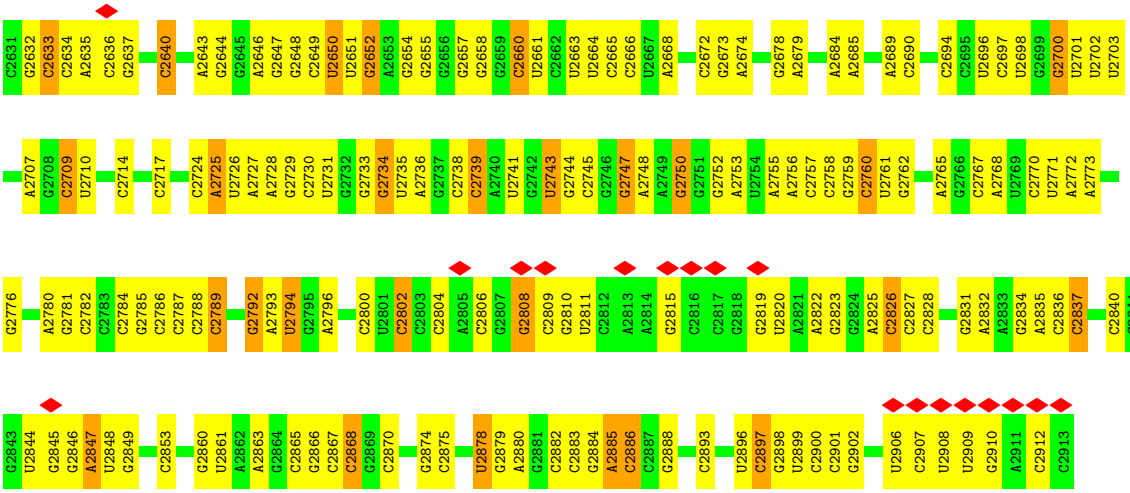
• Molecule 29: 23S ribosomal RNA

Chain A1:



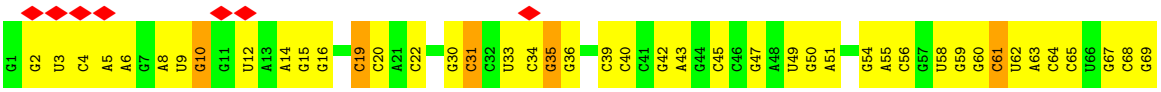


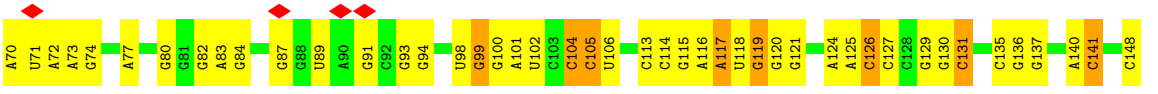


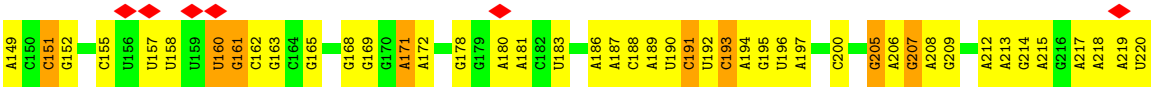


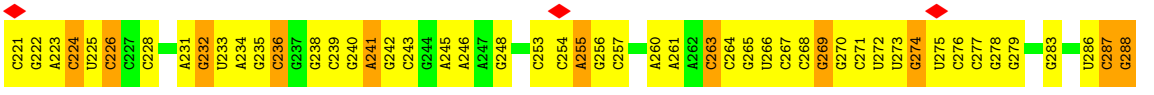
• Molecule 29: 23S ribosomal RNA

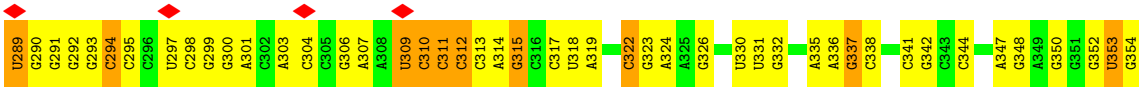
Chain A2:

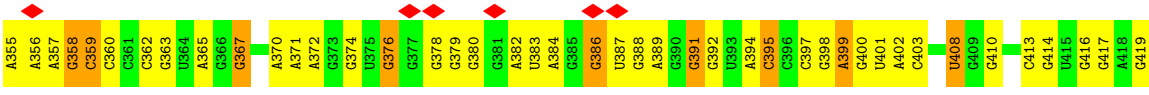


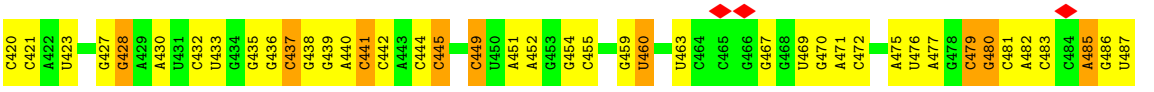


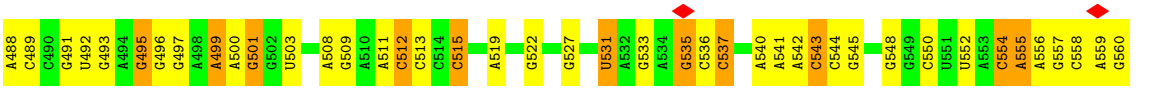


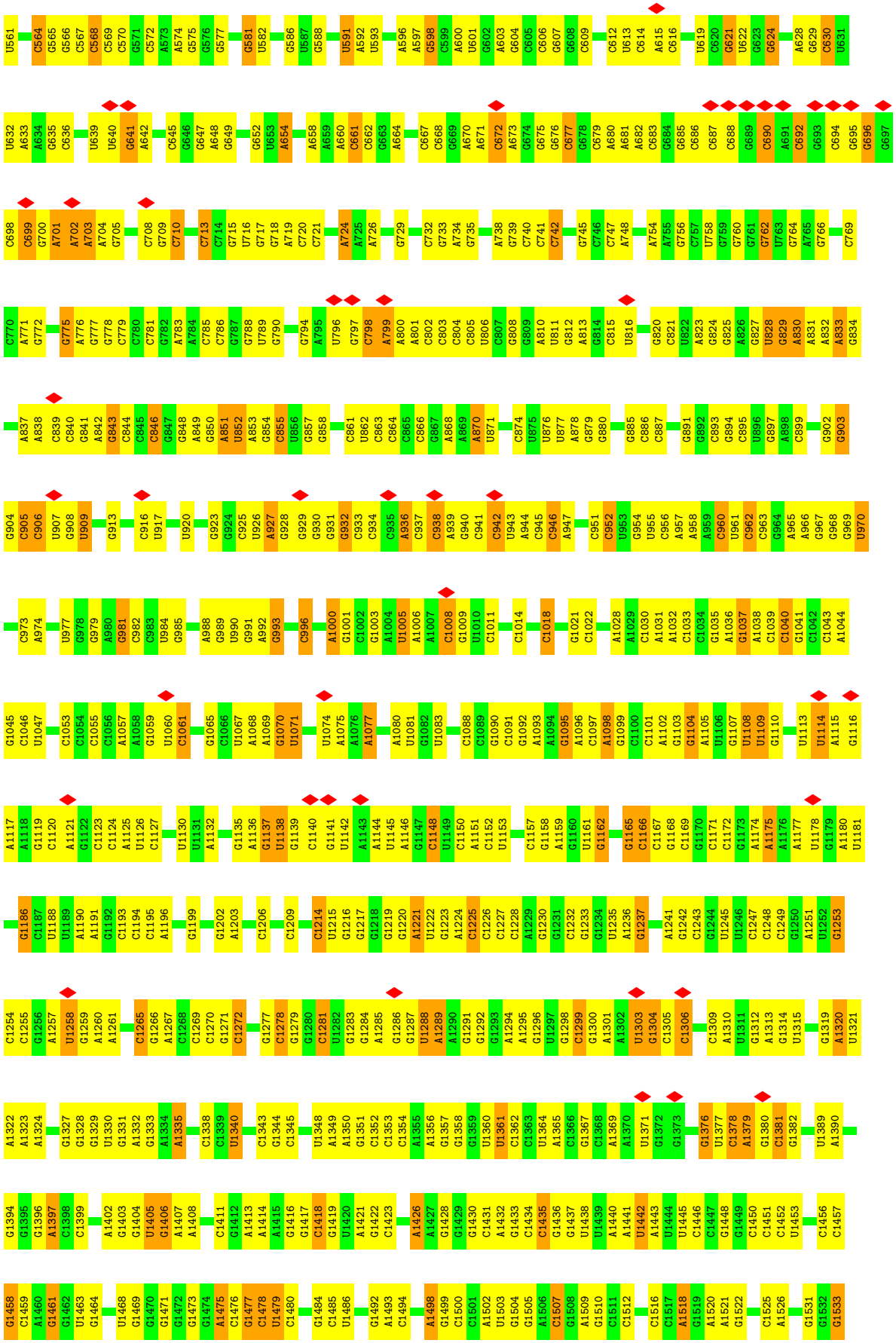


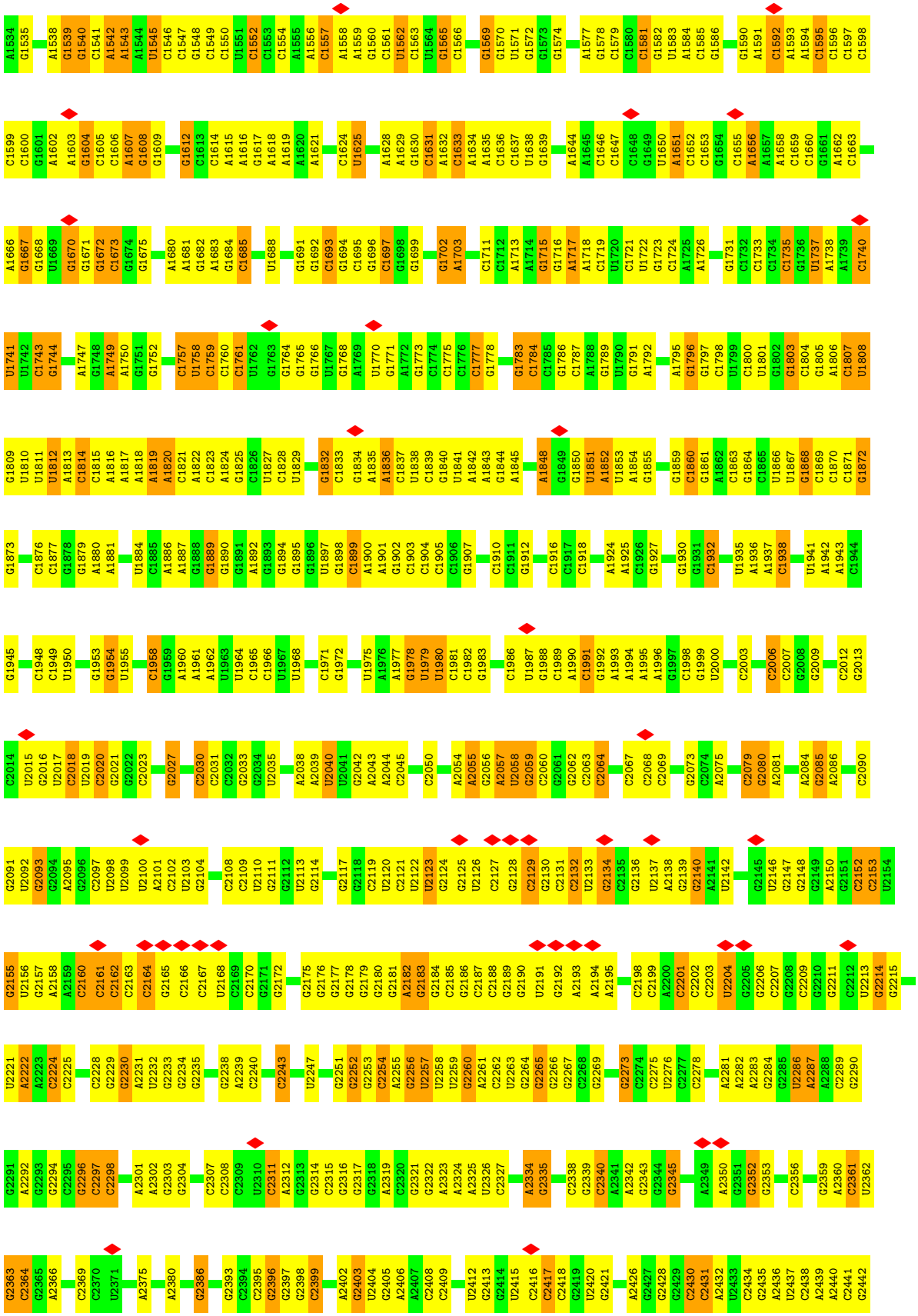


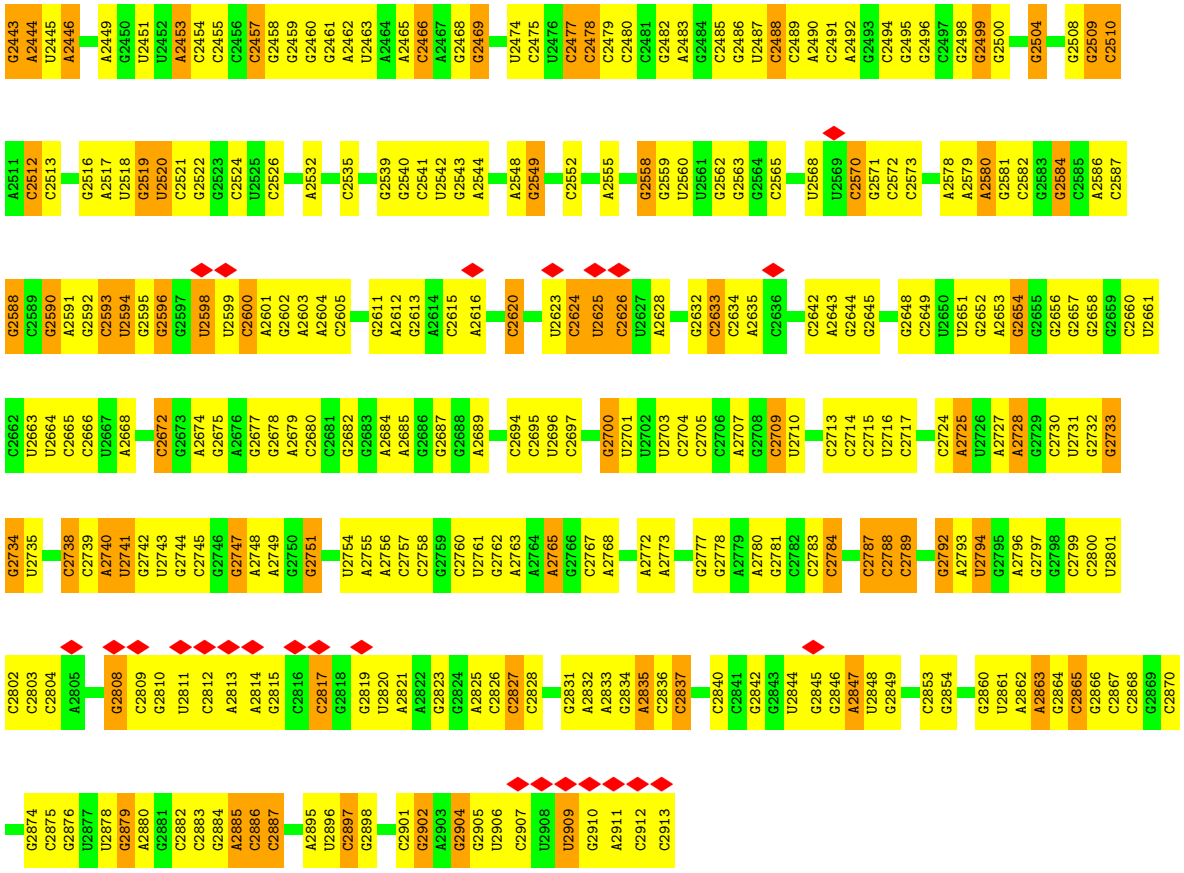






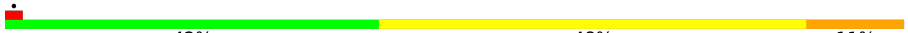


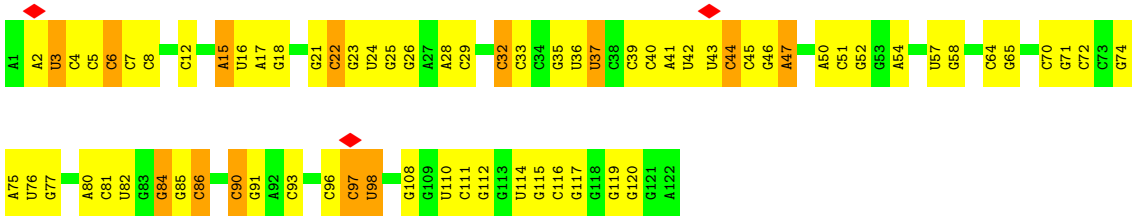




• Molecule 30: 5S ribosomal RNA

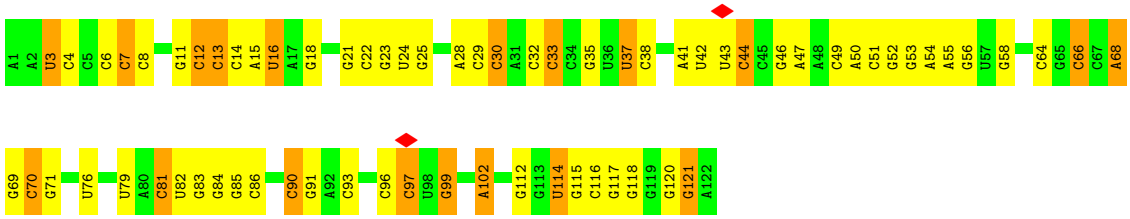
Chain B1:





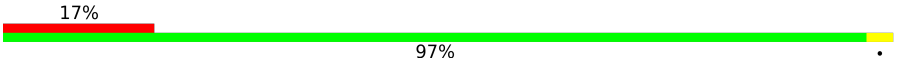
• Molecule 30: 5S ribosomal RNA

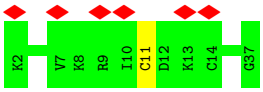
Chain B2:



• Molecule 31: 50S ribosomal protein L36

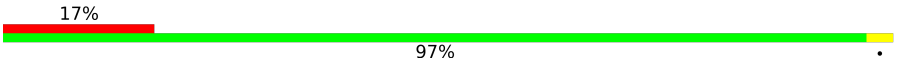
Chain e1:

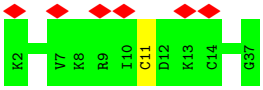




• Molecule 31: 50S ribosomal protein L36

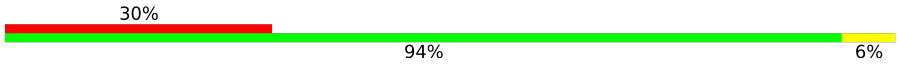
Chain e2:

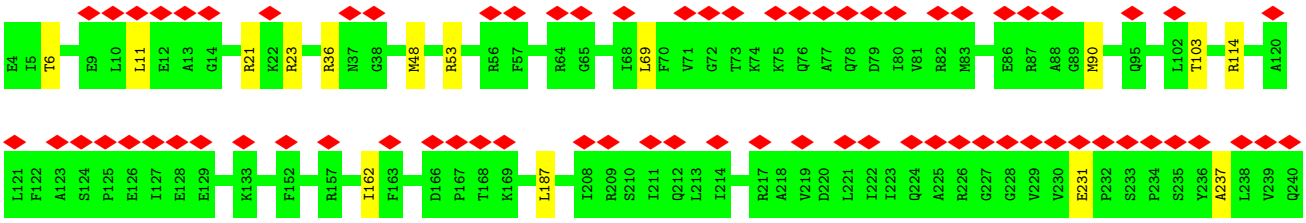




• Molecule 32: 30S ribosomal protein S2

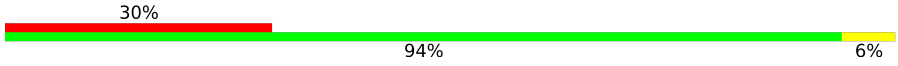
Chain B3:

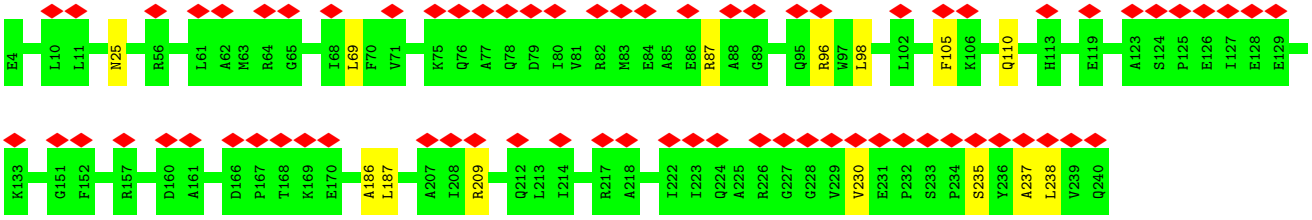




• Molecule 32: 30S ribosomal protein S2

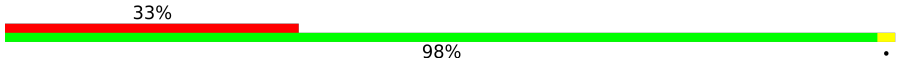
Chain B4:

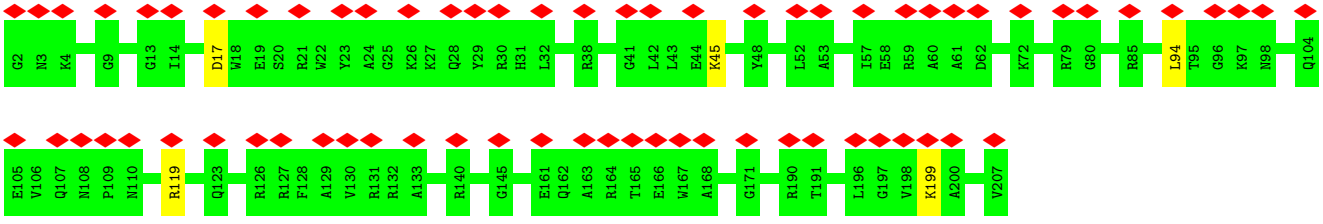




• Molecule 33: 30S ribosomal protein S3

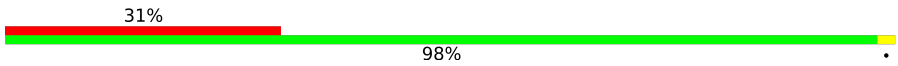
Chain C3:

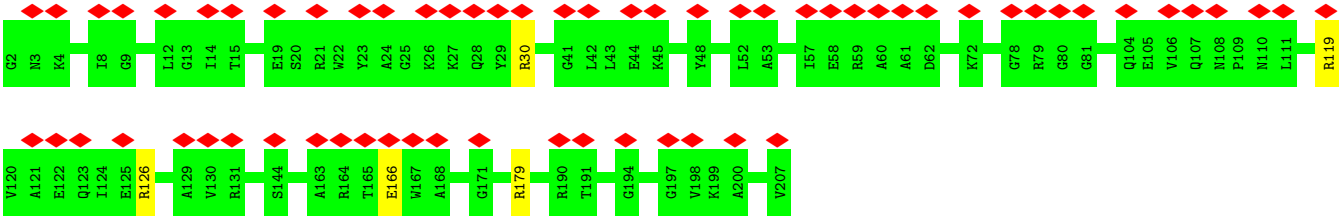




• Molecule 33: 30S ribosomal protein S3

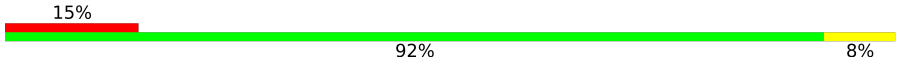
Chain C4:

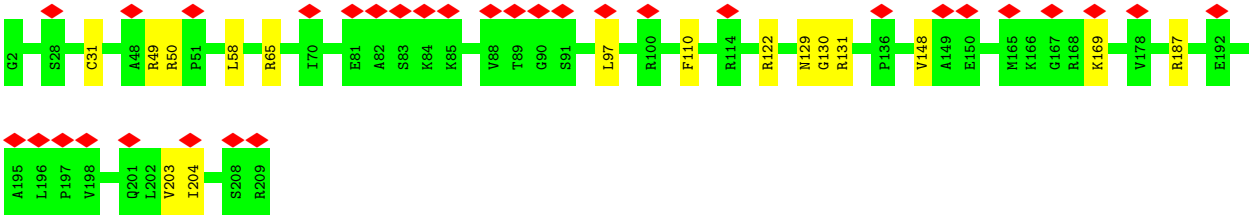




• Molecule 34: 30S ribosomal protein S4

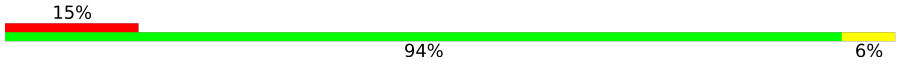
Chain D3:

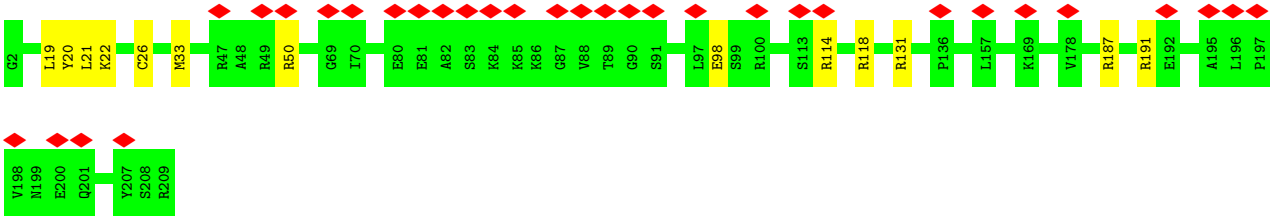




• Molecule 34: 30S ribosomal protein S4

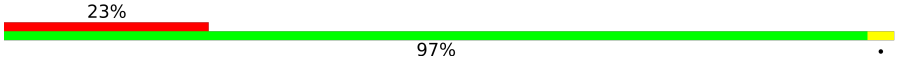
Chain D4:

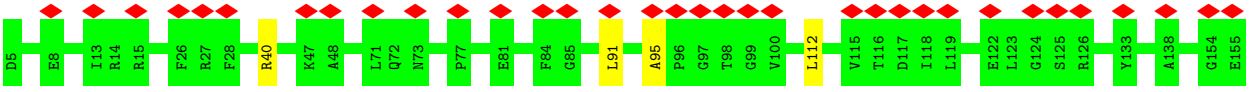




• Molecule 35: 30S ribosomal protein S5

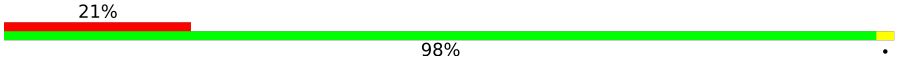
Chain E3:

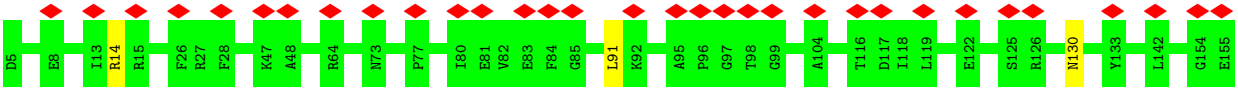




• Molecule 35: 30S ribosomal protein S5

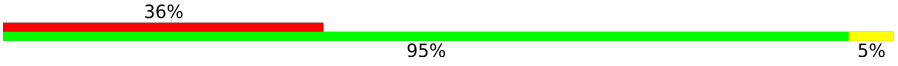
Chain E4:

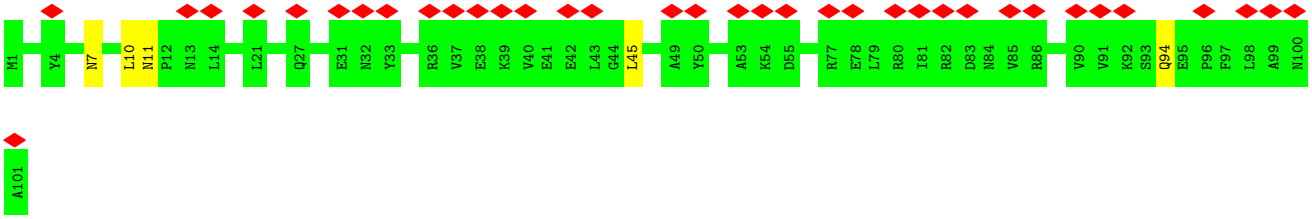




• Molecule 36: 30S ribosomal protein S6

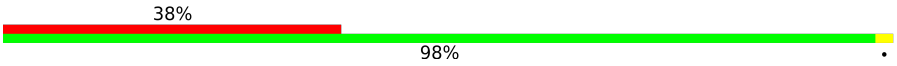
Chain F3:

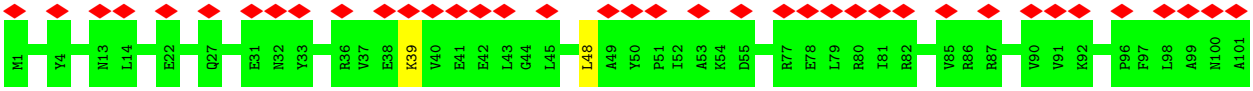




• Molecule 36: 30S ribosomal protein S6

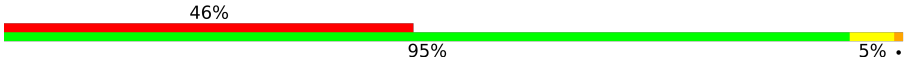
Chain F4:

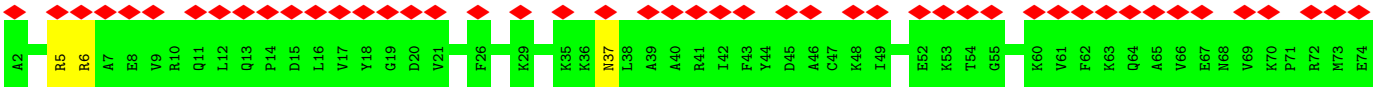


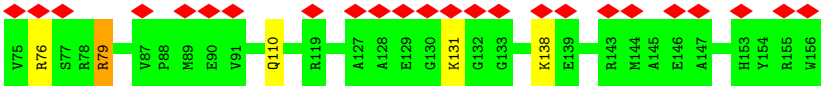


• Molecule 37: 30S ribosomal protein S7

Chain G3:

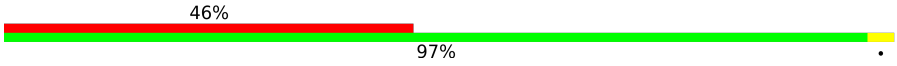


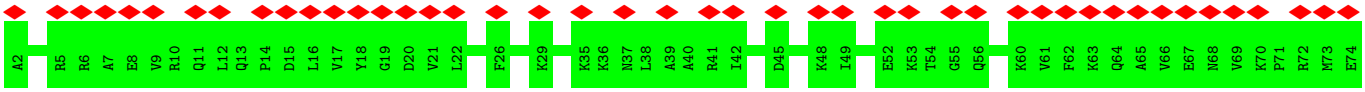


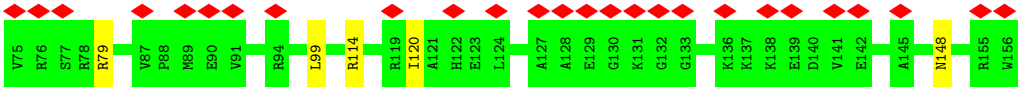


• Molecule 37: 30S ribosomal protein S7

Chain G4:

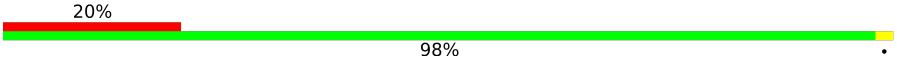


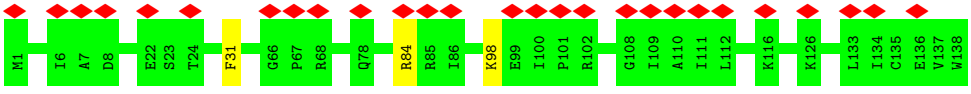




• Molecule 38: 30S ribosomal protein S8

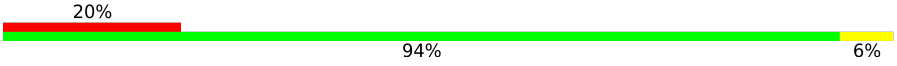
Chain H3:

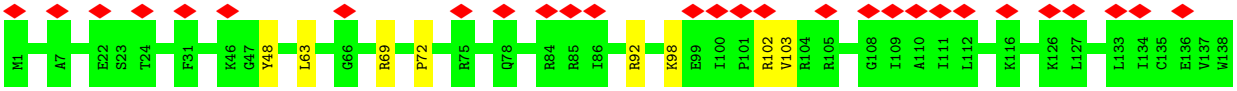




• Molecule 38: 30S ribosomal protein S8

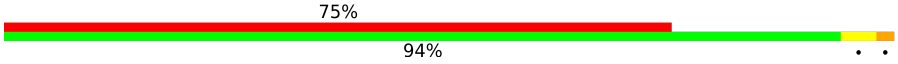
Chain H4:

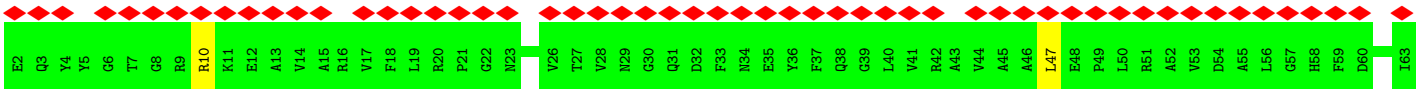


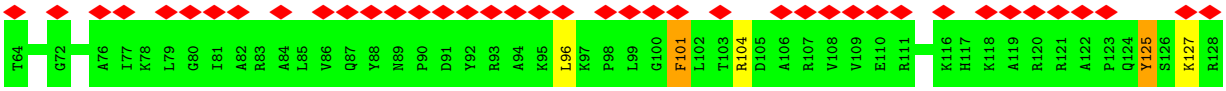


• Molecule 39: 30S ribosomal protein S9

Chain I3:

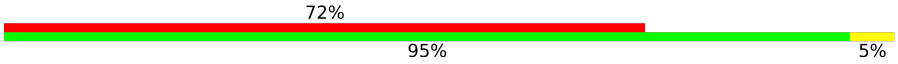


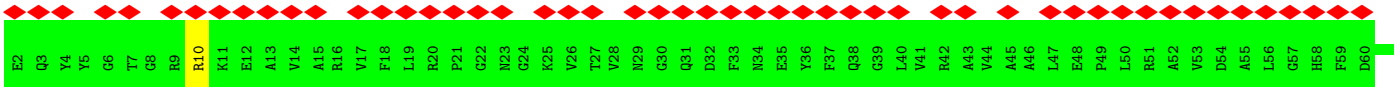


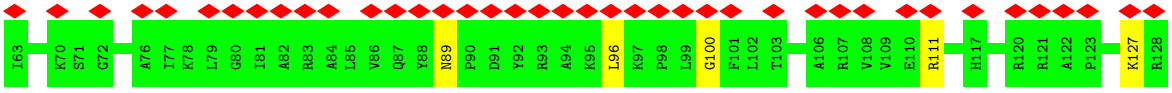


• Molecule 39: 30S ribosomal protein S9

Chain I4:

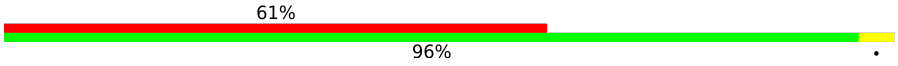


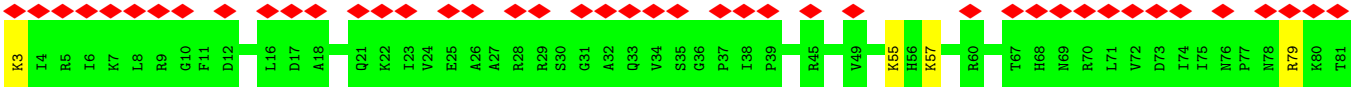


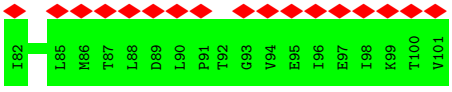


• Molecule 40: 30S ribosomal protein S10

Chain J3:

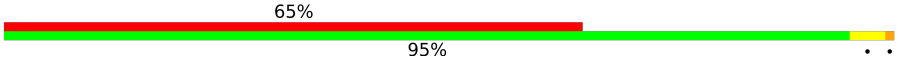


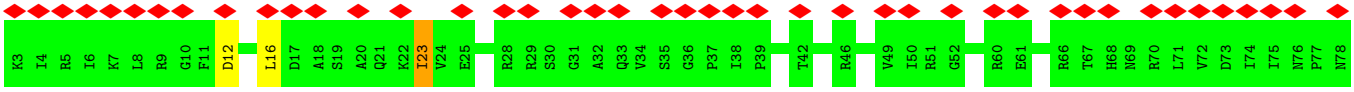


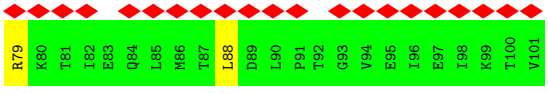


• Molecule 40: 30S ribosomal protein S10

Chain J4:

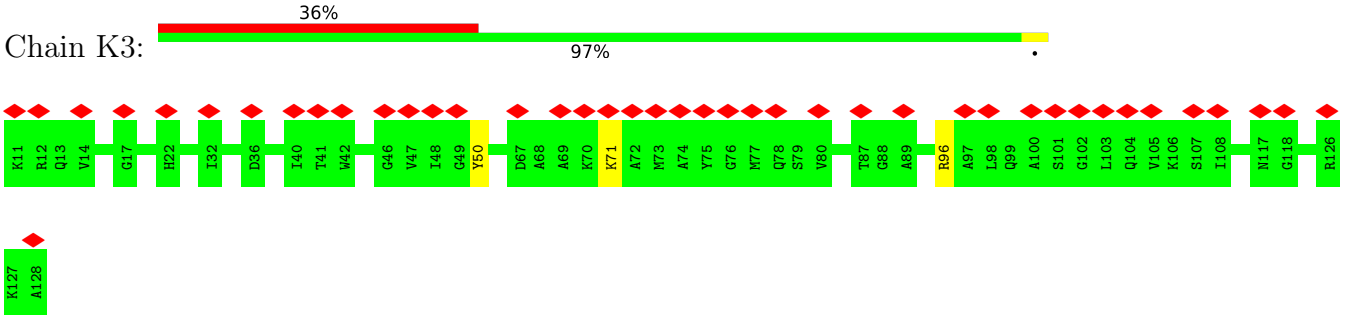






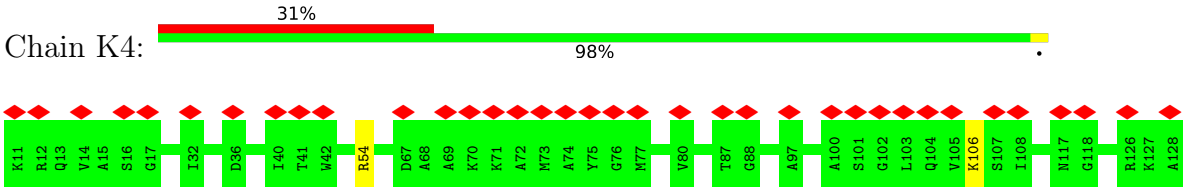
• Molecule 41: 30S ribosomal protein S11

Chain K3:



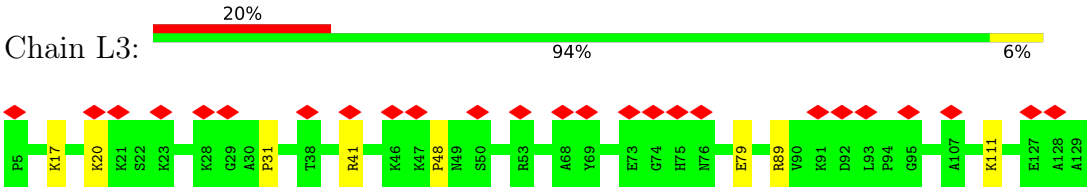
• Molecule 41: 30S ribosomal protein S11

Chain K4:



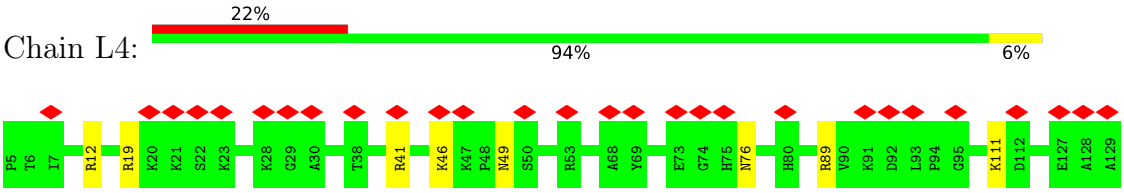
• Molecule 42: 30S ribosomal protein S12

Chain L3:



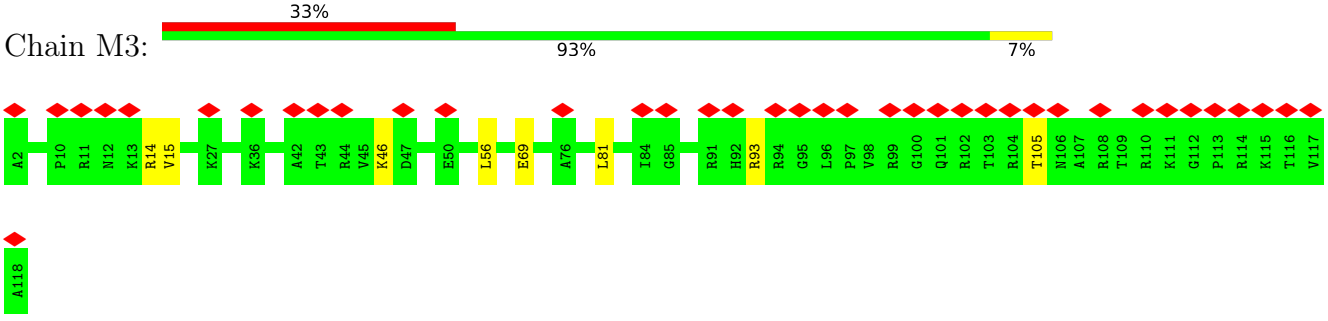
• Molecule 42: 30S ribosomal protein S12

Chain L4:



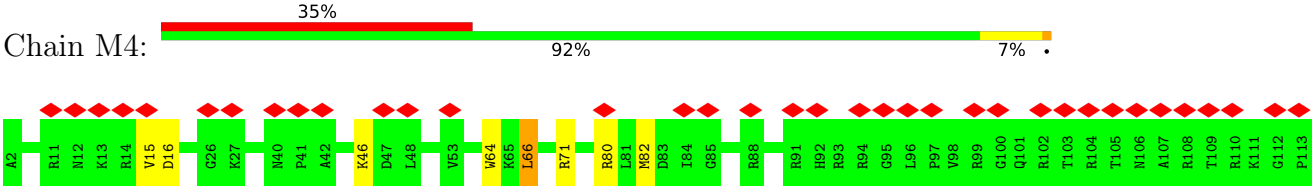
• Molecule 43: 30S ribosomal protein S13

Chain M3:



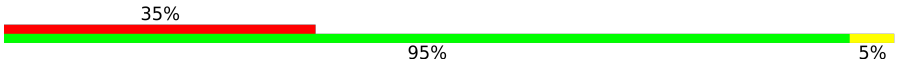
• Molecule 43: 30S ribosomal protein S13

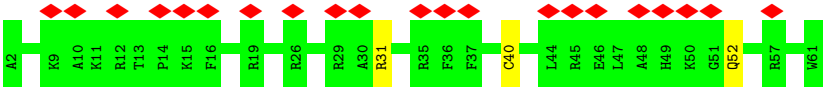
Chain M4:



• Molecule 44: 30S ribosomal protein S14 type Z

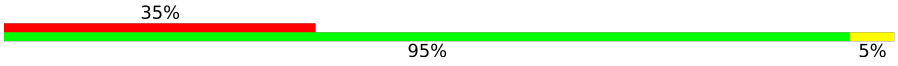
Chain N3:

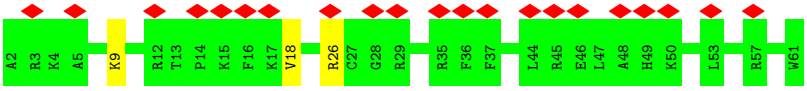




• Molecule 44: 30S ribosomal protein S14 type Z

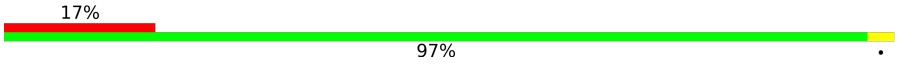
Chain N4:

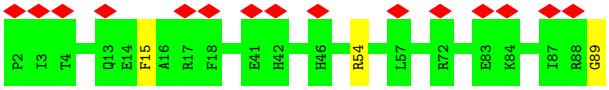




• Molecule 45: 30S ribosomal protein S15

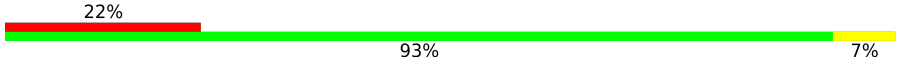
Chain O3:

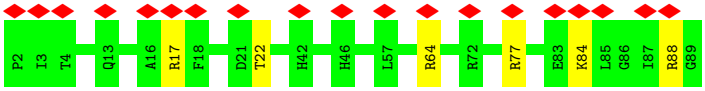




• Molecule 45: 30S ribosomal protein S15

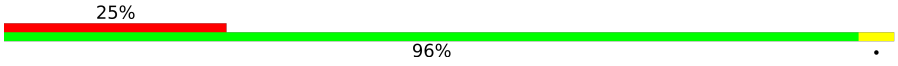
Chain O4:

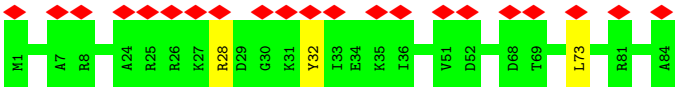




• Molecule 46: 30S ribosomal protein S16

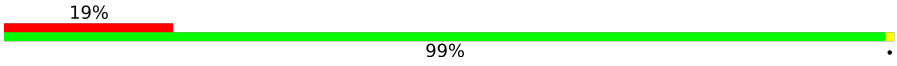
Chain P3:

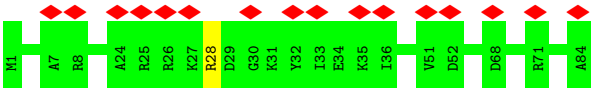




• Molecule 46: 30S ribosomal protein S16

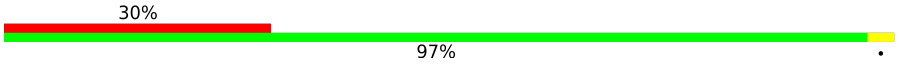
Chain P4:

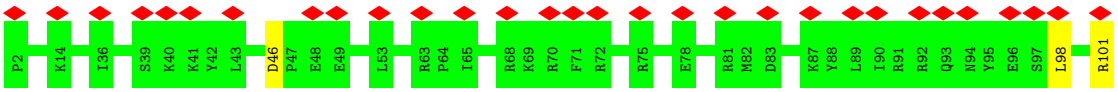




• Molecule 47: 30S ribosomal protein S17

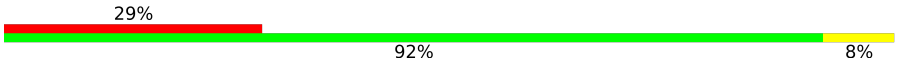
Chain Q3:

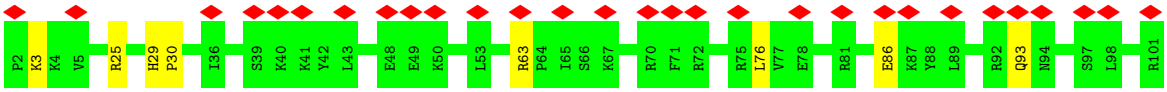




• Molecule 47: 30S ribosomal protein S17

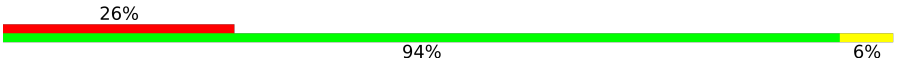
Chain Q4:

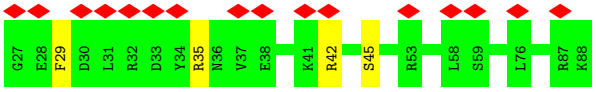




• Molecule 48: 30S ribosomal protein S18

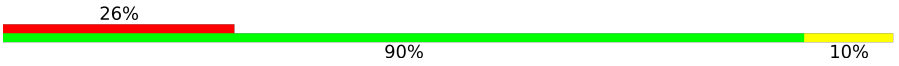
Chain R3:

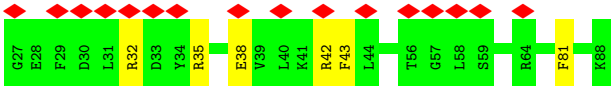




• Molecule 48: 30S ribosomal protein S18

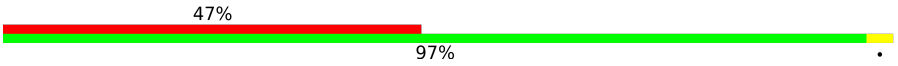
Chain R4:

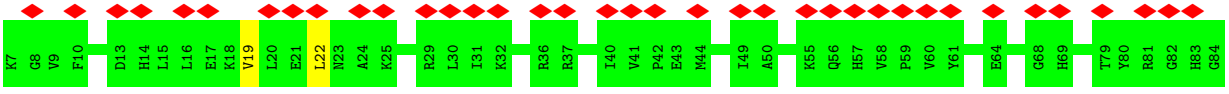




• Molecule 49: 30S ribosomal protein S19

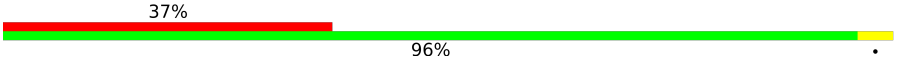
Chain S3:

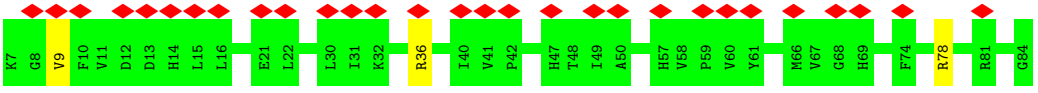




• Molecule 49: 30S ribosomal protein S19

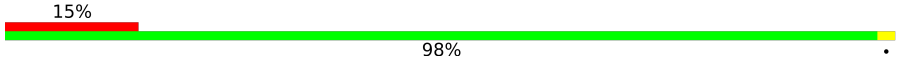
Chain S4:

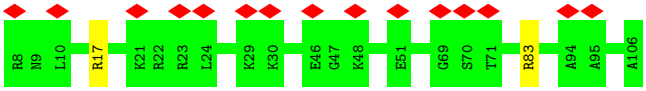




• Molecule 50: 30S ribosomal protein S20

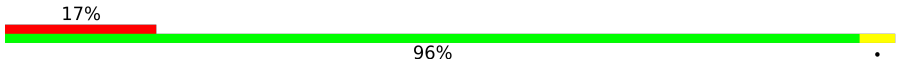
Chain T3:

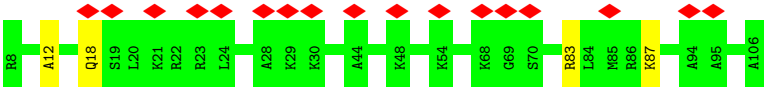




• Molecule 50: 30S ribosomal protein S20

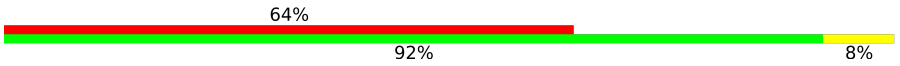
Chain T4:

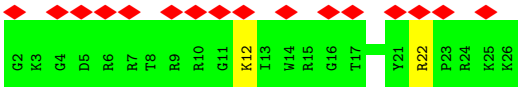




• Molecule 51: 30S ribosomal protein Thx

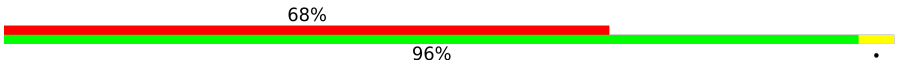
Chain U3:

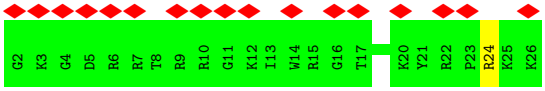




• Molecule 51: 30S ribosomal protein Thx

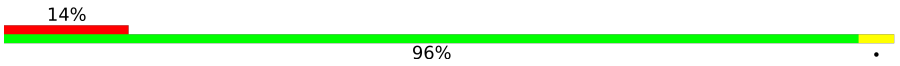
Chain U4:

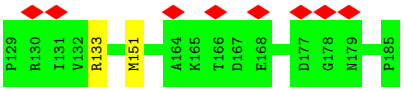




• Molecule 52: Ribosome hibernation promoting factor

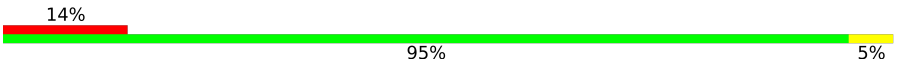
Chain X3:

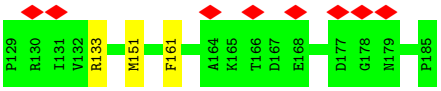




• Molecule 52: Ribosome hibernation promoting factor

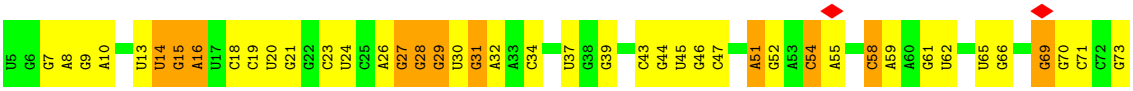
Chain W4:

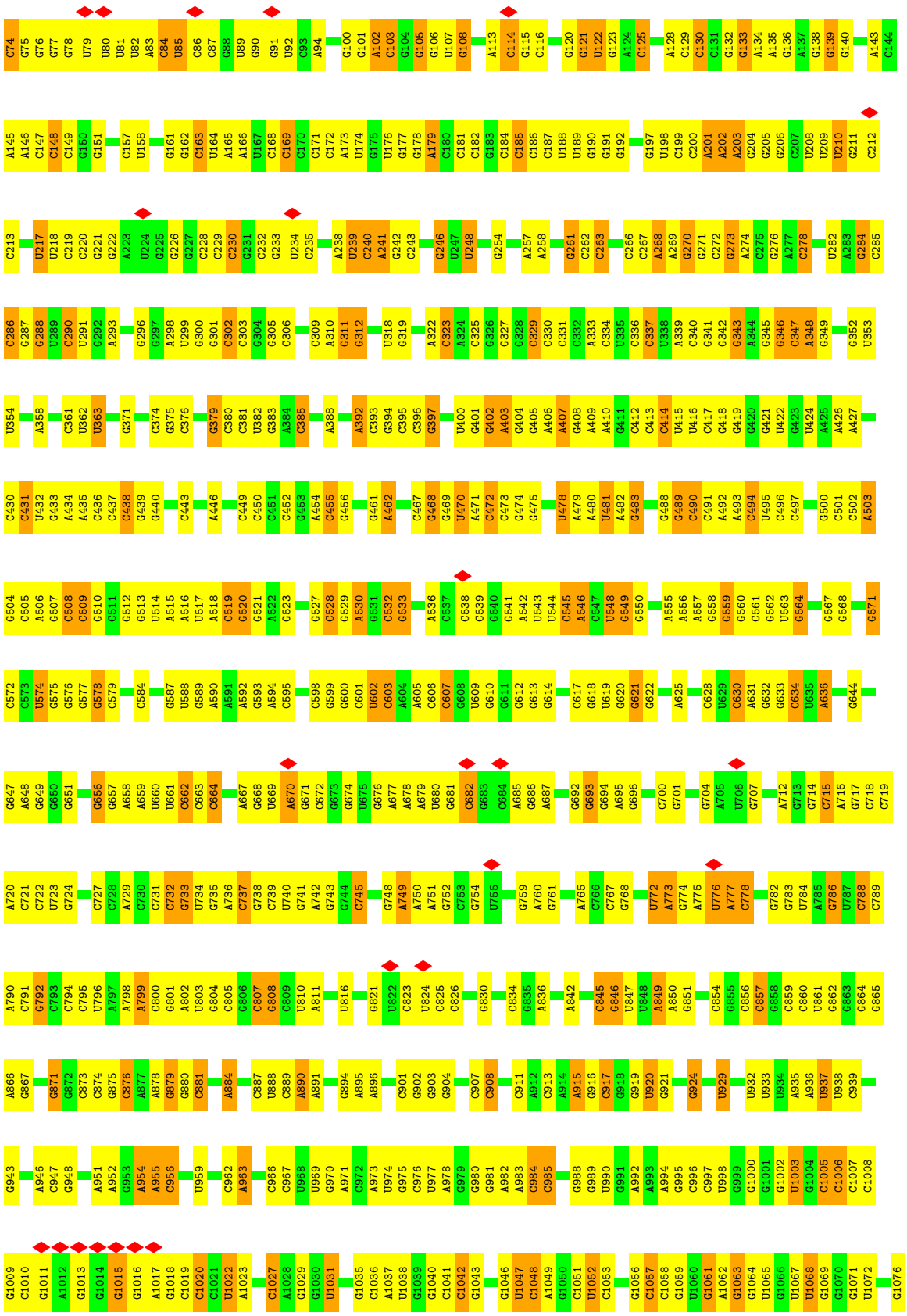


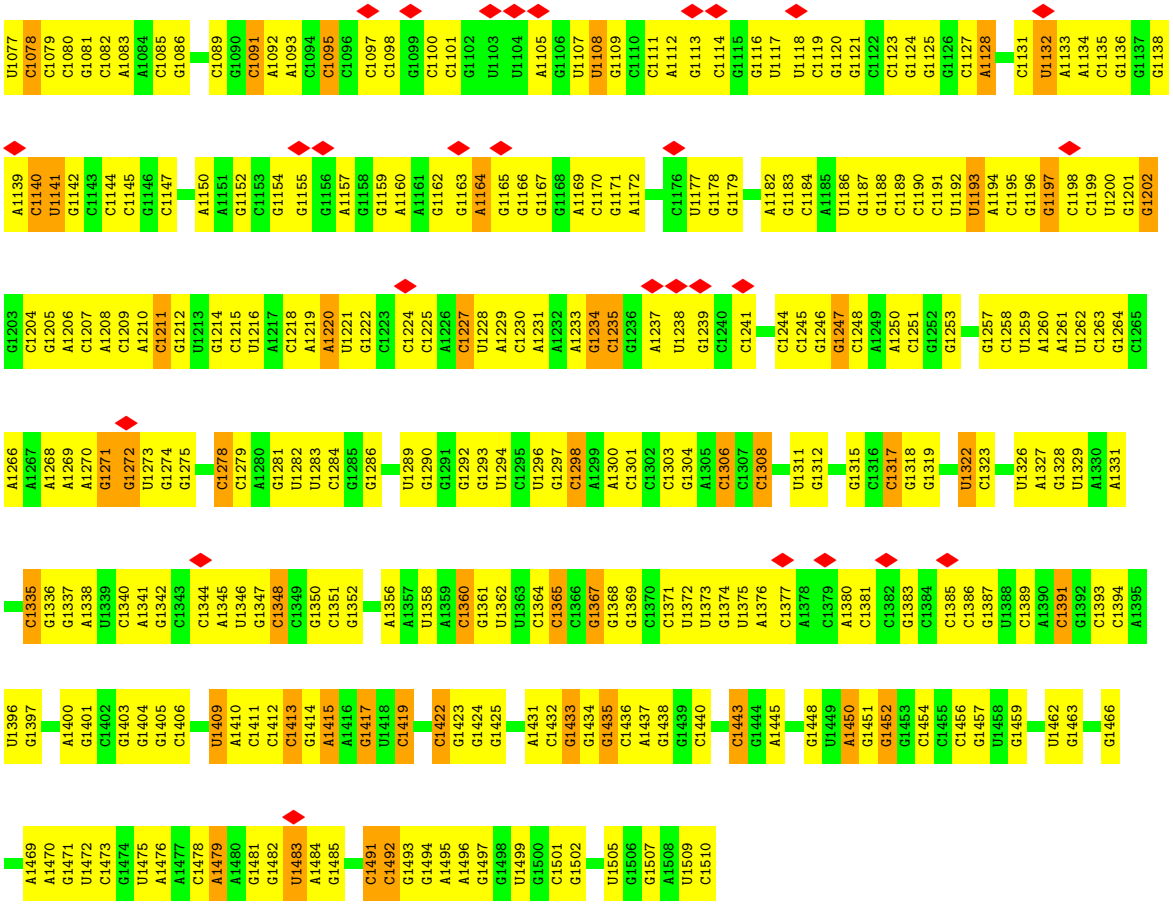


• Molecule 53: 16S ribosomal RNA

Chain A3:

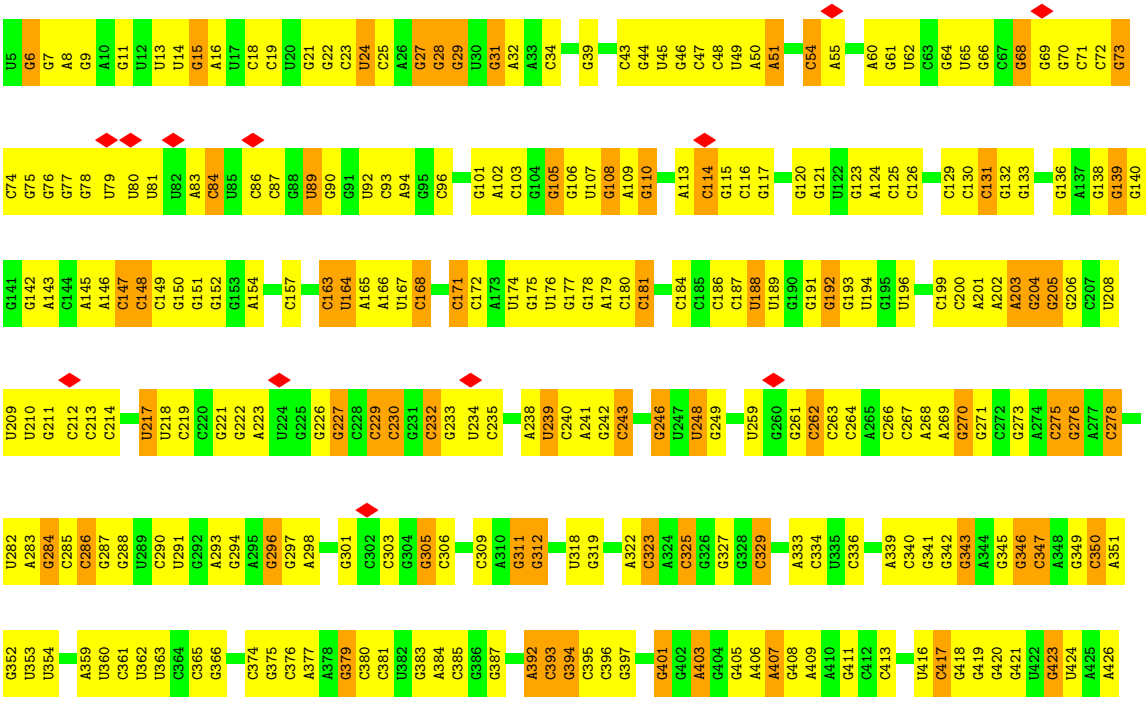


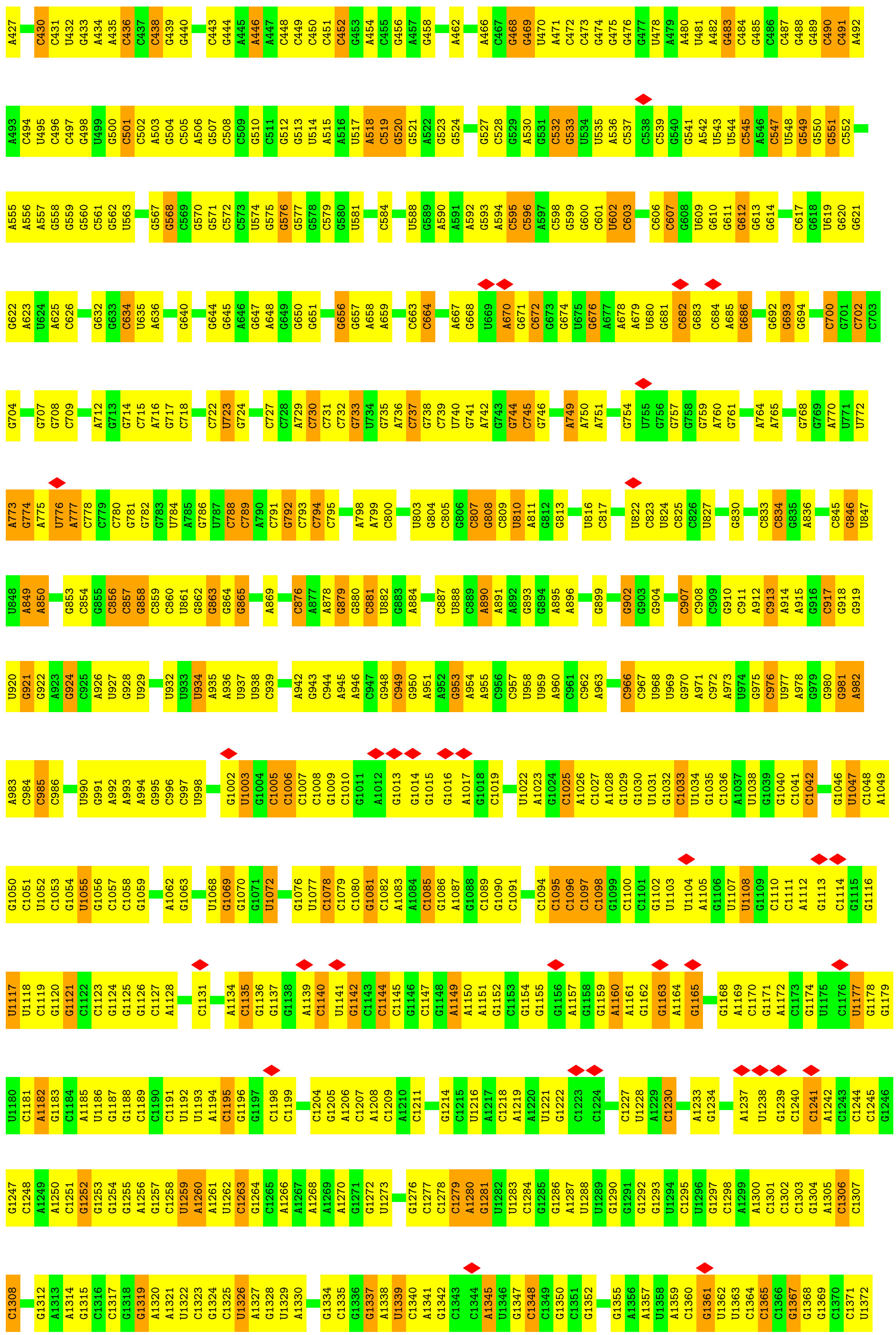

C74 G75 G76 G77 G78 U79 U80 U81 U82 A83 C84 U85 C86 C87 G88 U89 G90 G91 U92 C93 A94 G100 G101 A102 C103 G104 G105 G106 U107 G108 A113 C114 G115 C116 G120 G121 U122 G123 A124 C125 A128 C129 C130 C131 G132 G133 A134 A135 G136 A137 G138 G139 G140 A143 C144
A145 A146 C147 C148 C149 G150 G151 C157 U158 G161 G162 C163 U164 A165 A166 U167 C168 C169 C170 C171 C172 A173 U174 G175 U176 G177 G178 A179 C180 C181 C182 G183 C184 C185 C186 C187 U188 U189 G190 G191 G192 G197 U198 C199 C200 A201 A202 A203 G204 G205 G206 C207 U208 U209 U210 G211 C212
C213 U217 U218 C219 C220 G221 G222 A223 U224 G225 G226 G227 C228 C229 C230 G231 C232 G233 U234 C235 A238 U239 C240 A241 G242 C243 G246 U247 U248 G254 A257 A258 G261 C262 C263 C266 C267 A268 A269 G270 G271 C272 G273 A274 C275 G276 A277 C278 U282 A283 G284 C285
C286 G287 G288 U289 C290 U291 G292 A293 G296 G297 A298 U299 G300 G301 C302 C303 G304 G305 C306 C309 A310 G311 G312 U318 G319 A322 C323 A324 C325 G326 G327 G328 C329 C330 C331 C332 A333 C334 U335 C336 C337 U338 A339 C340 G341 G342 G343 A344 G345 G346 C347 A348 G349 G352 U353
U354 A358 C361 U362 U363 G371 C374 G375 C376 G379 C380 C381 U382 G383 A384 C385 A388 A392 C393 G394 C395 C396 G397 U400 G401 G402 A403 C404 G405 A406 A407 G408 A409 A410 G411 C412 C413 C414 U415 U416 C417 G418 A419 G420 G421 U422 G423 U424 A425 A426 A427
C430 C431 U432 G433 A434 A435 C436 C437 C438 G439 G440 C443 A446 C449 C450 C451 C452 G453 A454 C455 G456 G461 A462 C467 G468 G469 U470 A471 G472 C473 G474 G475 U478 A479 A480 U481 A482 G483 G488 G489 C490 C491 A492 A493 C494 U495 C496 C497 G500 C501 C502 A503
G504 C505 A506 G507 C508 C509 G510 C511 G512 G513 U514 A515 A516 U517 A518 C519 G520 G521 A522 G523 G527 C528 G529 A530 G531 C532 G533 A536 C537 C538 C539 G540 G541 A542 U543 U544 C545 A546 C547 U548 G549 G550 A555 A556 A557 G558 G559 G560 C561 G562 U563 G564 G567 G568 G571
C572 G573 U574 G575 G576 G577 G578 C579 C584 G587 U588 G589 A590 A591 A592 G593 A594 C595 C598 G599 G600 C601 U602 C603 A604 A605 C606 C607 G608 U609 G610 G611 G612 G613 G614 C617 G618 U619 G620 G621 G622 A625 C628 U629 C630 A631 G632 G633 C634 U635 A636 G644
G647 A648 G649 G650 G651 G656 G657 A658 A659 U660 U661 C662 C663 C664 A667 G668 U669 A670 G671 C672 G673 G674 U675 G676 A677 A678 A679 U680 G681 C682 G683 C684 A685 G686 A687 G692 G693 G694 A695 G696 C700 G701 G704 A705 U706 G707 A712 G713 G714 C715 A716 G717 C718 C719
A720 C721 C722 U723 G724 C727 C728 A729 C730 C731 C732 G733 U734 G735 A736 C737 G738 C739 U740 G741 A742 G743 G744 C745 G748 A749 A750 A751 G752 C753 G754 U755 G759 A760 G761 A765 C766 C767 G768 U772 A773 G774 A775 U776 A777 C778 G782 G783 U784 A785 G786 U787 C788 C789
A790 C791 G792 C793 C794 C795 U796 A797 A798 A799 C800 G801 A802 U803 G804 C805 G806 C807 G808 C809 U810 A811 U816 G821 U822 C823 U824 C825 C826 G830 C834 G835 A836 A842 C845 G846 U847 U848 A849 A850 G851 C854 G855 C856 C857 G858 C859 C860 U861 G862 G863 G864 G865
A866 G867 G871 G872 C873 C874 G875 C876 A877 A878 G879 G880 C881 A884 C887 U888 C889 A890 A891 G894 A895 A896 C901 G902 G903 G904 C907 C908 C911 A912 C913 A914 A915 G916 C917 G918 G919 U920 G921 G924 U929 U932 U933 U934 A935 A936 U937 G938 C939
G943 A946 C947 G948 A951 A952 G953 A954 A955 C956 U959 C962 A963 C966 C967 U968 U969 G970 A971 C972 A973 U974 G975 C976 U977 A978 G979 G980 G981 A982 A983 C984 C985 G988 G989 U990 G991 A992 A993 A994 G995 C996 C997 U998 G999 G1000 G1001 G1002 U1003 G1004 C1005 C1006 C1007 C1008
G1009 C1010 G1011 A1012 G1013 G1014 G1015 G1016 A1017 G1018 C1019 C1020 C1021 U1022 A1023 C1027 A1028 G1029 G1030 U1031 G1035 C1036 A1037 U1038 G1039 G1040 C1041 C1042 G1043 G1046 U1047 C1048 A1049 G1050 C1051 U1052 C1053 G1056 C1057 C1058 G1059 U1060 G1061 A1062 G1063 G1064 U1065 G1066 U1067 U1068 G1069 G1070 G1071 U1072 G1076

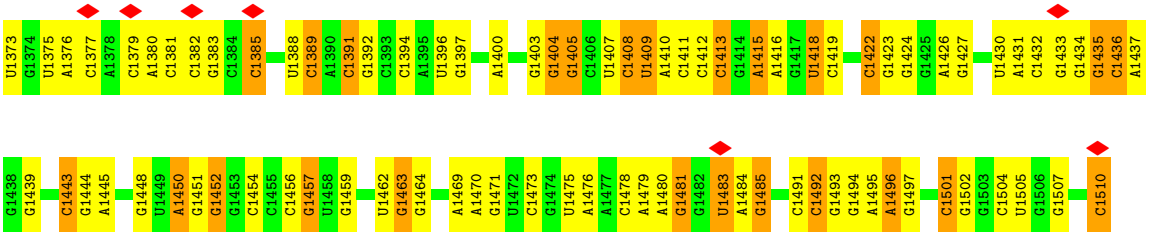


• Molecule 53: 16S ribosomal RNA

Chain A4:

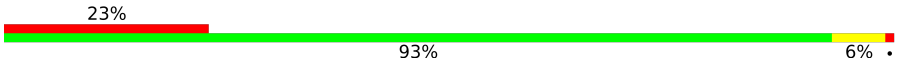


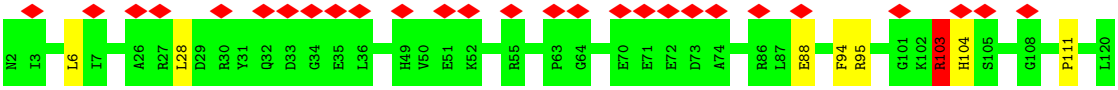

A427 C430 C431 U432 G433 A434 A435 C436 C437 C438 G439 G440 C443 G444 A445 A446 A447 C448 C449 C450 C451 C452 G453 A454 C455 G456 A457 G458 A462 A466 C467 G468 G469 U470 A471 C472 C473 G474 G475 G476 G477 U478 A479 A480 U481 A482 G483 C484 G485 C486 C487 G488 G489 C490 C491 A492
A493 C494 U495 C496 C497 G498 U499 G500 C501 C502 A503 G504 C505 A506 G507 C508 C509 G510 C511 G512 G513 U514 A515 A516 U517 A518 C519 G520 G521 A522 G523 G524 G527 C528 G529 A530 G531 C532 G533 U534 U535 A536 C537 C538 C539 G540 G541 A542 U543 U544 C545 A546 C547 U548 G549 G550 G551 C552
A555 A556 A557 G558 G559 G560 C561 G562 U563 G567 G568 C569 G570 G571 C572 C573 U574 G575 C576 G577 G578 C579 G580 U581 C584 U588 G589 A590 A591 A592 G593 A594 C595 C596 A597 C598 G599 G600 C601 U602 C603 C606 C607 G608 U609 G610 G611 C612 G613 G614 C617 G618 U619 G620 G621
G622 A623 U624 A625 C626 G632 G633 C634 U635 A636 G640 G644 G645 A646 G647 A648 G649 G650 G651 G656 G657 A658 A659 C663 C664 A667 G668 U669 A670 G671 C672 G673 G674 U675 G676 A677 A678 A679 U680 G681 C682 G683 C684 A685 G686 G692 G693 G694 C700 G701 C702 C703
G704 G707 G708 C709 A712 G713 G714 C715 A716 G717 C718 C722 U723 G724 C727 C728 A729 C730 C731 C732 G733 U734 G735 A736 C737 G738 C739 U740 G741 A742 G743 G744 C745 G746 A749 A750 A751 G754 U755 G756 G757 G758 G759 A760 G761 A764 A765 G768 G769 A770 U771 U772
A773 G774 A775 U776 A777 C778 C779 C780 G781 G782 G783 U784 A785 G786 U787 C788 C789 A790 C791 G792 C793 C794 C795 A798 A799 C800 U803 G804 C805 G806 C807 G808 C809 U810 A811 G812 G813 U816 C817 U822 C823 U824 C825 C826 U827 G830 C833 C834 G835 A836 C845 G846 U847
U848 A849 A850 G853 C854 G855 C856 C857 G858 C859 C860 U861 G862 G863 G864 G865 A869 C876 A877 A878 G879 G880 C881 U882 G883 A884 C887 U888 C889 A890 A891 A892 G893 G894 A895 A896 G899 G902 G903 G904 C907 C908 C909 G910 C911 A912 C913 A914 A915 G916 C917 G918 G919
U920 G921 G922 A923 G924 C925 A926 U927 G928 U929 U932 U933 U934 A935 A936 U937 U938 C939 A942 G943 C944 A945 A946 C947 G948 C949 G950 A951 A952 G953 A954 A955 C956 C957 U958 U959 A960 C961 C962 A963 C966 C967 U968 U969 G970 A971 C972 A973 U974 G975 C976 U977 A978 G979 G980 G981 A982
A983 C984 C985 C986 U990 G991 A992 A993 A994 G995 C996 C997 U998 G1002 U1003 G1004 C1005 C1006 C1007 C1008 G1009 C1010 G1011 A1012 G1013 G1014 U1015 G1016 A1017 G1018 C1019 U1022 A1023 G1024 C1025 A1026 C1027 A1028 G1029 G1030 U1031 G1032 C1033 U1034 G1035 C1036 A1037 U1038 G1039 G1040 C1041 C1042 G1046 U1047 C1048 A1049
G1050 C1051 U1052 C1053 G1054 U1055 G1056 C1057 C1058 G1059 A1062 G1063 U1068 G1069 G1070 G1071 U1072 G1076 U1077 C1078 C1079 C1080 G1081 C1082 A1083 A1084 C1085 G1086 A1087 G1088 C1089 G1090 C1091 C1094 C1095 C1096 C1097 C1098 G1099 C1100 C1101 G1102 U1103 U1104 A1105 G1106 U1107 U1108 G1109 C1110 C1111 A1112 G1113 C1114 G1115 G1116
U1117 U1118 C1119 G1120 G1121 C1122 C1123 G1124 G1125 G1126 C1127 A1128 C1131 A1134 C1135 G1136 G1137 G1138 A1139 C1140 U1141 G1142 C1143 C1144 C1145 G1146 C1147 G1148 A1149 A1150 A1151 C1152 C1153 G1154 G1155 G1156 A1157 G1158 G1159 A1160 A1161 G1162 G1163 A1164 G1165 G1168 A1169 C1170 G1171 A1172 C1173 G1174 U1175 C1176 U1177 G1178 G1179
U1180 C1181 A1182 G1183 C1184 A1185 U1186 G1187 G1188 C1189 C1190 C1191 U1192 U1193 A1194 C1195 G1196 G1197 C1198 C1199 C1204 G1205 A1206 C1207 A1208 C1209 A1210 C1211 G1214 C1215 U1216 A1217 C1218 A1219 A1220 U1221 G1222 C1223 C1224 C1227 U1228 A1229 C1230 A1233 G1234 A1237 U1238 G1239 C1240 C1241 A1242 C1243 C1244 C1245 G1246
G1247 C1248 A1249 A1250 C1251 G1252 G1253 G1254 G1255 A1256 G1257 C1258 U1259 A1260 A1261 U1262 C1263 G1264 C1265 A1266 A1267 A1268 A1269 A1270 G1271 G1272 U1273 G1276 C1277 C1278 C1279 A1280 G1281 U1282 U1283 C1284 G1285 G1286 A1287 U1288 U1289 G1290 G1291 G1292 G1293 U1294 C1295 U1296 G1297 C1298 A1299 A1300 C1301 C1302 C1303 G1304 A1305 C1306 C1307
C1308 G1312 A1313 A1314 G1315 C1316 C1317 G1318 G1319 A1320 A1321 U1322 C1323 C1324 C1325 U1326 A1327 G1328 U1329 A1330 G1334 C1335 G1336 G1337 A1338 U1339 C1340 A1341 G1342 C1343 C1344 A1345 U1346 G1347 C1348 C1349 G1350 C1351 G1352 G1355 A1356 A1357 U1358 A1359 C1360 G1361 U1362 U1363 C1364 C1365 C1366 G1367 G1368 G1369 C1370 C1371 U1372



• Molecule 54: Ribosome hibernation promoting factor

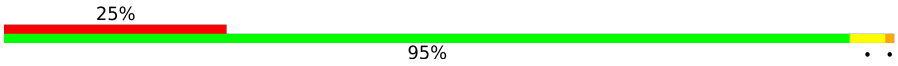
Chain V3:

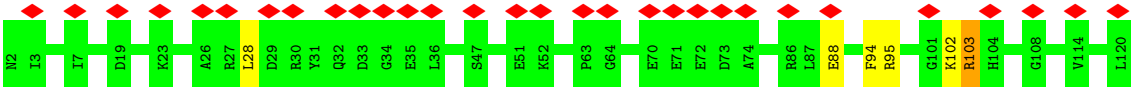




• Molecule 54: Ribosome hibernation promoting factor

Chain V4:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25368	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 ($e^-/Å^2$)	1.06	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	11.760	Depositor
Minimum map value	-5.930	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.355	Depositor
Recommended contour level	2.3	Depositor
Map size (Å)	770.0, 770.0, 770.0	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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	C1	0.57	1/2166 (0.0%)	0.77	0/2919
1	C2	0.55	0/2166	0.77	2/2919 (0.1%)
2	D1	0.49	0/1602	0.77	0/2160
2	D2	0.49	0/1602	0.71	0/2160
3	E1	0.52	1/1663 (0.1%)	0.74	0/2249
3	E2	0.50	0/1663	0.75	0/2249
4	F1	0.46	0/1499	0.76	1/2016 (0.0%)
4	F2	0.44	0/1499	0.78	3/2016 (0.1%)
5	G1	0.42	0/1333	0.73	0/1802
5	G2	0.44	0/1333	0.74	1/1802 (0.1%)
6	H1	0.43	0/387	0.73	0/523
6	H2	0.42	0/387	0.79	0/523
7	I1	0.45	0/1132	0.68	0/1525
7	I2	0.45	0/1132	0.73	1/1525 (0.1%)
8	J1	0.55	0/943	0.73	0/1269
8	J2	0.54	0/943	0.71	0/1269
9	K1	0.47	0/1162	0.84	0/1544
9	K2	0.44	0/1162	0.80	1/1544 (0.1%)
10	L1	0.54	0/1143	0.75	0/1527
10	L2	0.53	0/1143	0.70	0/1527
11	M1	0.43	0/974	0.78	0/1302
11	M2	0.44	0/974	0.73	1/1302 (0.1%)
12	N1	0.44	0/892	0.79	0/1187
12	N2	0.42	0/892	0.76	0/1187
13	O1	0.52	0/1156	0.76	1/1542 (0.1%)
13	O2	0.53	0/1156	0.76	1/1542 (0.1%)
14	P1	0.41	0/982	0.71	1/1306 (0.1%)
14	P2	0.42	0/982	0.71	1/1306 (0.1%)
15	Q1	0.46	0/790	0.72	0/1057
15	Q2	0.44	0/790	0.75	0/1057
16	R1	0.44	0/911	0.74	1/1220 (0.1%)
16	R2	0.45	0/911	0.74	3/1220 (0.2%)
17	S1	0.48	0/740	0.76	0/993
17	S2	0.46	0/740	0.74	0/993

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
18	T1	0.41	0/799	0.73	0/1064
18	T2	0.40	0/799	0.72	0/1064
19	U1	0.42	0/1461	0.73	1/1982 (0.1%)
19	U2	0.44	0/1461	0.71	0/1982
20	V1	0.45	0/621	0.74	0/827
20	V2	0.46	0/621	0.74	0/827
21	W1	0.48	0/770	0.85	1/1022 (0.1%)
21	W2	0.47	0/770	0.72	0/1022
22	X1	0.40	0/583	0.69	0/771
22	X2	0.43	0/583	0.72	0/771
23	Y1	0.41	0/474	0.77	1/635 (0.2%)
23	Y2	0.41	0/474	0.74	0/635
24	Z1	0.48	0/528	0.84	0/709
24	Z2	0.50	0/528	0.88	1/709 (0.1%)
25	a1	0.45	0/473	0.70	0/639
25	a2	0.47	0/473	0.72	0/639
26	b1	0.48	0/397	0.76	0/529
26	b2	0.51	0/397	0.86	0/529
27	c1	0.60	1/438 (0.2%)	0.71	0/575
27	c2	0.55	0/438	0.68	0/575
28	d1	0.48	0/495	0.82	1/649 (0.2%)
28	d2	0.52	0/495	0.85	0/649
29	A1	1.43	52/70233 (0.1%)	1.57	1459/109643 (1.3%)
29	A2	1.08	52/70233 (0.1%)	1.58	1543/109643 (1.4%)
30	B1	0.87	1/2928 (0.0%)	1.44	38/4568 (0.8%)
30	B2	0.87	0/2928	1.48	61/4568 (1.3%)
31	e1	0.49	0/302	0.67	0/397
31	e2	0.49	0/302	0.68	0/397
32	B3	0.48	0/1960	0.82	5/2642 (0.2%)
32	B4	0.47	0/1960	0.76	4/2642 (0.2%)
33	C3	0.47	0/1637	0.74	0/2205
33	C4	0.48	0/1637	0.78	0/2205
34	D3	0.50	0/1731	0.79	1/2312 (0.0%)
34	D4	0.47	0/1733	0.80	0/2318
35	E3	0.47	0/1172	0.78	3/1576 (0.2%)
35	E4	0.45	0/1172	0.75	1/1576 (0.1%)
36	F3	0.50	0/856	0.76	1/1154 (0.1%)
36	F4	0.52	0/856	0.75	0/1154
37	G3	0.47	0/1276	0.71	0/1709
37	G4	0.46	0/1276	0.71	1/1709 (0.1%)
38	H3	0.48	0/1136	0.74	0/1527
38	H4	0.47	0/1136	0.75	0/1527
39	I3	0.49	0/1029	0.82	4/1379 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
39	I4	0.46	0/1029	0.78	2/1379 (0.1%)
40	J3	0.42	0/815	0.72	0/1095
40	J4	0.42	0/815	0.75	2/1095 (0.2%)
41	K3	0.49	0/894	0.71	0/1205
41	K4	0.49	0/894	0.74	0/1205
42	L3	0.49	0/992	0.80	2/1327 (0.2%)
42	L4	0.50	0/992	0.76	0/1327
43	M3	0.41	0/944	0.75	0/1265
43	M4	0.44	0/944	0.92	5/1265 (0.4%)
44	N3	0.45	0/501	0.75	0/664
44	N4	0.45	0/501	0.74	0/664
45	O3	3.89	1/745 (0.1%)	0.81	1/992 (0.1%)
45	O4	0.44	0/745	0.77	0/992
46	P3	0.47	0/722	0.74	0/970
46	P4	0.42	0/722	0.69	0/970
47	Q3	0.50	0/848	0.78	2/1131 (0.2%)
47	Q4	0.51	0/848	0.81	1/1131 (0.1%)
48	R3	0.47	0/520	0.79	0/690
48	R4	0.48	0/520	0.77	0/690
49	S3	0.46	0/639	0.77	1/860 (0.1%)
49	S4	0.44	0/639	0.76	0/860
50	T3	0.41	0/765	0.70	0/1007
50	T4	0.39	0/765	0.70	0/1007
51	U3	0.37	0/222	0.81	0/288
51	U4	0.38	0/222	0.83	0/288
52	W4	0.49	0/487	0.80	0/650
52	X3	0.50	0/487	0.81	0/650
53	A3	1.05	25/36234 (0.1%)	1.60	792/56554 (1.4%)
53	A4	1.05	28/36234 (0.1%)	1.61	839/56554 (1.5%)
54	V3	0.51	0/977	0.82	1/1316 (0.1%)
54	V4	0.51	0/977	0.81	1/1316 (0.1%)
All	All	1.04	162/314160 (0.1%)	1.40	4793/469344 (1.0%)

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
1	C1	0	6
1	C2	0	6
2	D1	0	4

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D2	0	2
3	E1	0	1
3	E2	0	2
4	F1	0	6
4	F2	0	4
5	G2	0	1
6	H1	0	1
7	I1	0	2
7	I2	0	2
8	J1	0	2
8	J2	0	2
9	K1	0	2
9	K2	0	1
11	M2	0	1
12	N1	0	2
12	N2	0	1
13	O1	0	2
13	O2	0	3
14	P1	0	1
14	P2	0	3
15	Q2	0	2
16	R1	0	1
16	R2	0	5
17	S2	0	1
18	T1	0	1
18	T2	0	1
19	U1	0	1
19	U2	0	4
20	V1	0	1
20	V2	0	1
21	W1	0	3
21	W2	0	1
22	X1	0	1
22	X2	0	2
24	Z1	0	8
24	Z2	0	1
25	a2	0	1
26	b1	0	2
26	b2	0	2
27	c1	0	1
28	d1	0	2
28	d2	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
31	e1	0	1
31	e2	0	1
32	B3	0	7
32	B4	0	6
33	C3	0	1
33	C4	0	1
34	D3	0	8
34	D4	0	5
35	E3	0	1
35	E4	0	1
36	F3	0	2
36	F4	0	1
37	G3	0	3
37	G4	0	3
38	H3	0	1
38	H4	0	4
39	I3	0	2
40	J3	0	1
40	J4	0	3
41	K3	0	2
42	L3	0	3
42	L4	0	3
43	M3	0	4
43	M4	0	2
44	N3	0	2
44	N4	0	2
45	O3	0	1
46	P3	0	2
47	Q4	0	5
48	R3	0	2
48	R4	0	3
49	S3	0	1
50	T3	0	2
50	T4	0	2
51	U3	0	1
51	U4	0	1
52	W4	0	1
54	V3	0	2
54	V4	0	1
All	All	0	194

The worst 5 of 162 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	A1	764	G	C8-N7	128.76	2.08	1.30
29	A1	764	G	N7-C5	125.41	2.14	1.39
29	A1	764	G	N9-C8	112.11	2.16	1.37
45	O3	89	GLY	C-OXT	105.47	3.23	1.23
29	A1	764	G	N9-C4	95.43	2.14	1.38

The worst 5 of 4793 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
29	A1	764	G	N7-C8-N9	-24.77	100.72	113.10
29	A1	764	G	C5-N7-C8	17.48	113.04	104.30
29	A1	764	G	C6-N1-C2	17.13	135.38	125.10
29	A1	764	G	N3-C4-C5	-14.98	121.11	128.60
29	A1	764	G	C8-N9-C4	14.82	112.33	106.40

There are no chirality outliers.

5 of 194 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C1	13	ARG	Peptide
1	C1	178	PRO	Peptide
1	C1	51	VAL	Peptide
1	C1	67	PHE	Peptide
1	C1	86	PRO	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C1	270/272 (99%)	208 (77%)	62 (23%)	0	100	100
1	C2	270/272 (99%)	214 (79%)	56 (21%)	0	100	100
2	D1	203/205 (99%)	159 (78%)	44 (22%)	0	100	100
2	D2	203/205 (99%)	153 (75%)	48 (24%)	2 (1%)	13	49
3	E1	206/208 (99%)	157 (76%)	48 (23%)	1 (0%)	25	64
3	E2	206/208 (99%)	148 (72%)	57 (28%)	1 (0%)	25	64
4	F1	179/181 (99%)	141 (79%)	38 (21%)	0	100	100
4	F2	179/181 (99%)	139 (78%)	40 (22%)	0	100	100
5	G1	168/170 (99%)	126 (75%)	42 (25%)	0	100	100
5	G2	168/170 (99%)	130 (77%)	38 (23%)	0	100	100
6	H1	48/50 (96%)	37 (77%)	11 (23%)	0	100	100
6	H2	48/50 (96%)	36 (75%)	12 (25%)	0	100	100
7	I1	136/138 (99%)	113 (83%)	22 (16%)	1 (1%)	19	56
7	I2	136/138 (99%)	112 (82%)	24 (18%)	0	100	100
8	J1	120/122 (98%)	98 (82%)	22 (18%)	0	100	100
8	J2	120/122 (98%)	93 (78%)	27 (22%)	0	100	100
9	K1	148/150 (99%)	119 (80%)	29 (20%)	0	100	100
9	K2	148/150 (99%)	106 (72%)	42 (28%)	0	100	100
10	L1	139/141 (99%)	107 (77%)	32 (23%)	0	100	100
10	L2	139/141 (99%)	104 (75%)	35 (25%)	0	100	100
11	M1	115/117 (98%)	100 (87%)	15 (13%)	0	100	100
11	M2	115/117 (98%)	100 (87%)	15 (13%)	0	100	100
12	N1	109/111 (98%)	87 (80%)	22 (20%)	0	100	100
12	N2	109/111 (98%)	86 (79%)	23 (21%)	0	100	100
13	O1	135/137 (98%)	105 (78%)	30 (22%)	0	100	100
13	O2	135/137 (98%)	96 (71%)	39 (29%)	0	100	100
14	P1	115/117 (98%)	96 (84%)	19 (16%)	0	100	100
14	P2	115/117 (98%)	102 (89%)	13 (11%)	0	100	100
15	Q1	99/101 (98%)	79 (80%)	20 (20%)	0	100	100
15	Q2	99/101 (98%)	72 (73%)	27 (27%)	0	100	100
16	R1	111/113 (98%)	96 (86%)	15 (14%)	0	100	100
16	R2	111/113 (98%)	91 (82%)	20 (18%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	S1	90/92 (98%)	73 (81%)	17 (19%)	0	100	100
17	S2	90/92 (98%)	74 (82%)	16 (18%)	0	100	100
18	T1	100/102 (98%)	76 (76%)	23 (23%)	1 (1%)	13	49
18	T2	100/102 (98%)	80 (80%)	19 (19%)	1 (1%)	13	49
19	U1	177/179 (99%)	140 (79%)	37 (21%)	0	100	100
19	U2	177/179 (99%)	141 (80%)	36 (20%)	0	100	100
20	V1	75/77 (97%)	63 (84%)	12 (16%)	0	100	100
20	V2	75/77 (97%)	61 (81%)	14 (19%)	0	100	100
21	W1	95/97 (98%)	73 (77%)	22 (23%)	0	100	100
21	W2	95/97 (98%)	69 (73%)	26 (27%)	0	100	100
22	X1	67/69 (97%)	53 (79%)	14 (21%)	0	100	100
22	X2	67/69 (97%)	55 (82%)	12 (18%)	0	100	100
23	Y1	57/59 (97%)	46 (81%)	11 (19%)	0	100	100
23	Y2	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
24	Z1	61/63 (97%)	31 (51%)	28 (46%)	2 (3%)	3	21
24	Z2	61/63 (97%)	36 (59%)	23 (38%)	2 (3%)	3	21
25	a1	57/59 (97%)	45 (79%)	12 (21%)	0	100	100
25	a2	57/59 (97%)	46 (81%)	11 (19%)	0	100	100
26	b1	43/45 (96%)	30 (70%)	13 (30%)	0	100	100
26	b2	43/45 (96%)	29 (67%)	14 (33%)	0	100	100
27	c1	47/49 (96%)	39 (83%)	8 (17%)	0	100	100
27	c2	47/49 (96%)	38 (81%)	9 (19%)	0	100	100
28	d1	59/61 (97%)	38 (64%)	21 (36%)	0	100	100
28	d2	59/61 (97%)	41 (70%)	18 (30%)	0	100	100
31	e1	34/36 (94%)	27 (79%)	7 (21%)	0	100	100
31	e2	34/36 (94%)	28 (82%)	6 (18%)	0	100	100
32	B3	235/237 (99%)	170 (72%)	65 (28%)	0	100	100
32	B4	235/237 (99%)	186 (79%)	49 (21%)	0	100	100
33	C3	204/206 (99%)	158 (78%)	46 (22%)	0	100	100
33	C4	204/206 (99%)	153 (75%)	51 (25%)	0	100	100
34	D3	202/208 (97%)	171 (85%)	30 (15%)	1 (0%)	25	64

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	D4	206/208 (99%)	156 (76%)	50 (24%)	0	100	100
35	E3	149/151 (99%)	117 (78%)	32 (22%)	0	100	100
35	E4	149/151 (99%)	122 (82%)	27 (18%)	0	100	100
36	F3	99/101 (98%)	82 (83%)	17 (17%)	0	100	100
36	F4	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
37	G3	153/155 (99%)	125 (82%)	28 (18%)	0	100	100
37	G4	153/155 (99%)	130 (85%)	23 (15%)	0	100	100
38	H3	136/138 (99%)	115 (85%)	21 (15%)	0	100	100
38	H4	136/138 (99%)	110 (81%)	25 (18%)	1 (1%)	19	56
39	I3	125/127 (98%)	96 (77%)	29 (23%)	0	100	100
39	I4	125/127 (98%)	101 (81%)	24 (19%)	0	100	100
40	J3	97/99 (98%)	74 (76%)	23 (24%)	0	100	100
40	J4	97/99 (98%)	79 (81%)	18 (19%)	0	100	100
41	K3	116/118 (98%)	90 (78%)	26 (22%)	0	100	100
41	K4	116/118 (98%)	88 (76%)	28 (24%)	0	100	100
42	L3	123/125 (98%)	93 (76%)	29 (24%)	1 (1%)	16	54
42	L4	123/125 (98%)	96 (78%)	26 (21%)	1 (1%)	16	54
43	M3	115/117 (98%)	85 (74%)	30 (26%)	0	100	100
43	M4	115/117 (98%)	91 (79%)	24 (21%)	0	100	100
44	N3	58/60 (97%)	46 (79%)	12 (21%)	0	100	100
44	N4	58/60 (97%)	45 (78%)	13 (22%)	0	100	100
45	O3	86/88 (98%)	67 (78%)	19 (22%)	0	100	100
45	O4	86/88 (98%)	71 (83%)	15 (17%)	0	100	100
46	P3	82/84 (98%)	64 (78%)	18 (22%)	0	100	100
46	P4	82/84 (98%)	68 (83%)	14 (17%)	0	100	100
47	Q3	98/100 (98%)	80 (82%)	18 (18%)	0	100	100
47	Q4	98/100 (98%)	74 (76%)	24 (24%)	0	100	100
48	R3	60/62 (97%)	45 (75%)	15 (25%)	0	100	100
48	R4	60/62 (97%)	47 (78%)	13 (22%)	0	100	100
49	S3	76/78 (97%)	53 (70%)	23 (30%)	0	100	100
49	S4	76/78 (97%)	59 (78%)	17 (22%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
50	T3	97/99 (98%)	83 (86%)	14 (14%)	0	100 100
50	T4	97/99 (98%)	83 (86%)	14 (14%)	0	100 100
51	U3	23/25 (92%)	15 (65%)	8 (35%)	0	100 100
51	U4	23/25 (92%)	16 (70%)	7 (30%)	0	100 100
52	W4	55/57 (96%)	39 (71%)	16 (29%)	0	100 100
52	X3	55/57 (96%)	39 (71%)	16 (29%)	0	100 100
54	V3	117/119 (98%)	89 (76%)	26 (22%)	2 (2%)	7 36
54	V4	117/119 (98%)	89 (76%)	26 (22%)	2 (2%)	7 36
All	All	11542/11750 (98%)	9036 (78%)	2487 (22%)	19 (0%)	45 78

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
54	V3	103	ARG
54	V3	104	HIS
38	H4	103	VAL
3	E1	10	PRO
24	Z1	43	TYR

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C1	214/214 (100%)	209 (98%)	5 (2%)	45 64
1	C2	214/214 (100%)	209 (98%)	5 (2%)	45 64
2	D1	165/165 (100%)	164 (99%)	1 (1%)	84 88
2	D2	165/165 (100%)	165 (100%)	0	100 100
3	E1	165/165 (100%)	160 (97%)	5 (3%)	36 56
3	E2	165/165 (100%)	163 (99%)	2 (1%)	67 79
4	F1	155/155 (100%)	147 (95%)	8 (5%)	19 41
4	F2	155/155 (100%)	151 (97%)	4 (3%)	41 60

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	G1	142/142 (100%)	134 (94%)	8 (6%)	17	39
5	G2	142/142 (100%)	138 (97%)	4 (3%)	38	58
6	H1	41/41 (100%)	41 (100%)	0	100	100
6	H2	41/41 (100%)	41 (100%)	0	100	100
7	I1	117/117 (100%)	115 (98%)	2 (2%)	56	72
7	I2	117/117 (100%)	112 (96%)	5 (4%)	25	47
8	J1	100/100 (100%)	98 (98%)	2 (2%)	50	68
8	J2	100/100 (100%)	98 (98%)	2 (2%)	50	68
9	K1	116/116 (100%)	114 (98%)	2 (2%)	56	72
9	K2	116/116 (100%)	115 (99%)	1 (1%)	75	83
10	L1	111/111 (100%)	109 (98%)	2 (2%)	54	71
10	L2	111/111 (100%)	110 (99%)	1 (1%)	75	83
11	M1	100/100 (100%)	98 (98%)	2 (2%)	50	68
11	M2	100/100 (100%)	96 (96%)	4 (4%)	27	48
12	N1	87/87 (100%)	85 (98%)	2 (2%)	45	64
12	N2	87/87 (100%)	85 (98%)	2 (2%)	45	64
13	O1	120/120 (100%)	113 (94%)	7 (6%)	17	38
13	O2	120/120 (100%)	117 (98%)	3 (2%)	42	62
14	P1	93/93 (100%)	89 (96%)	4 (4%)	25	47
14	P2	93/93 (100%)	92 (99%)	1 (1%)	70	80
15	Q1	82/82 (100%)	80 (98%)	2 (2%)	44	63
15	Q2	82/82 (100%)	79 (96%)	3 (4%)	29	51
16	R1	92/92 (100%)	90 (98%)	2 (2%)	47	65
16	R2	92/92 (100%)	92 (100%)	0	100	100
17	S1	74/74 (100%)	73 (99%)	1 (1%)	62	75
17	S2	74/74 (100%)	71 (96%)	3 (4%)	26	48
18	T1	85/85 (100%)	81 (95%)	4 (5%)	22	44
18	T2	85/85 (100%)	83 (98%)	2 (2%)	44	63
19	U1	158/158 (100%)	156 (99%)	2 (1%)	65	77
19	U2	158/158 (100%)	154 (98%)	4 (2%)	42	62
20	V1	62/62 (100%)	60 (97%)	2 (3%)	34	54

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
20	V2	62/62 (100%)	60 (97%)	2 (3%)	34 54
21	W1	82/82 (100%)	81 (99%)	1 (1%)	67 79
21	W2	82/82 (100%)	79 (96%)	3 (4%)	29 51
22	X1	64/64 (100%)	63 (98%)	1 (2%)	58 74
22	X2	64/64 (100%)	64 (100%)	0	100 100
23	Y1	51/51 (100%)	51 (100%)	0	100 100
23	Y2	51/51 (100%)	51 (100%)	0	100 100
24	Z1	57/57 (100%)	56 (98%)	1 (2%)	54 71
24	Z2	57/57 (100%)	57 (100%)	0	100 100
25	a1	51/51 (100%)	51 (100%)	0	100 100
25	a2	51/51 (100%)	50 (98%)	1 (2%)	50 68
26	b1	44/44 (100%)	41 (93%)	3 (7%)	13 34
26	b2	44/44 (100%)	40 (91%)	4 (9%)	7 24
27	c1	42/42 (100%)	41 (98%)	1 (2%)	44 63
27	c2	42/42 (100%)	41 (98%)	1 (2%)	44 63
28	d1	51/51 (100%)	50 (98%)	1 (2%)	50 68
28	d2	51/51 (100%)	51 (100%)	0	100 100
31	e1	33/33 (100%)	33 (100%)	0	100 100
31	e2	33/33 (100%)	33 (100%)	0	100 100
32	B3	205/205 (100%)	201 (98%)	4 (2%)	50 68
32	B4	205/205 (100%)	201 (98%)	4 (2%)	50 68
33	C3	160/160 (100%)	156 (98%)	4 (2%)	42 62
33	C4	160/160 (100%)	156 (98%)	4 (2%)	42 62
34	D3	180/180 (100%)	174 (97%)	6 (3%)	33 54
34	D4	180/180 (100%)	172 (96%)	8 (4%)	24 46
35	E3	116/116 (100%)	115 (99%)	1 (1%)	75 83
35	E4	116/116 (100%)	115 (99%)	1 (1%)	75 83
36	F3	90/90 (100%)	88 (98%)	2 (2%)	47 65
36	F4	90/90 (100%)	89 (99%)	1 (1%)	70 80
37	G3	126/126 (100%)	120 (95%)	6 (5%)	21 43
37	G4	126/126 (100%)	125 (99%)	1 (1%)	79 84

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
38	H3	119/119 (100%)	117 (98%)	2 (2%)	56 72
38	H4	119/119 (100%)	116 (98%)	3 (2%)	42 62
39	I3	98/98 (100%)	95 (97%)	3 (3%)	35 55
39	I4	98/98 (100%)	94 (96%)	4 (4%)	26 48
40	J3	89/89 (100%)	86 (97%)	3 (3%)	32 53
40	J4	89/89 (100%)	88 (99%)	1 (1%)	70 80
41	K3	89/89 (100%)	88 (99%)	1 (1%)	70 80
41	K4	89/89 (100%)	87 (98%)	2 (2%)	47 65
42	L3	104/104 (100%)	101 (97%)	3 (3%)	37 57
42	L4	104/104 (100%)	100 (96%)	4 (4%)	28 49
43	M3	94/94 (100%)	90 (96%)	4 (4%)	25 47
43	M4	94/94 (100%)	90 (96%)	4 (4%)	25 47
44	N3	49/49 (100%)	48 (98%)	1 (2%)	50 68
44	N4	49/49 (100%)	48 (98%)	1 (2%)	50 68
45	O3	79/79 (100%)	78 (99%)	1 (1%)	65 77
45	O4	79/79 (100%)	73 (92%)	6 (8%)	11 30
46	P3	72/72 (100%)	71 (99%)	1 (1%)	62 75
46	P4	72/72 (100%)	71 (99%)	1 (1%)	62 75
47	Q3	95/95 (100%)	94 (99%)	1 (1%)	70 80
47	Q4	95/95 (100%)	93 (98%)	2 (2%)	48 67
48	R3	55/55 (100%)	53 (96%)	2 (4%)	30 51
48	R4	55/55 (100%)	52 (94%)	3 (6%)	18 40
49	S3	67/67 (100%)	67 (100%)	0	100 100
49	S4	67/67 (100%)	64 (96%)	3 (4%)	23 46
50	T3	76/76 (100%)	76 (100%)	0	100 100
50	T4	76/76 (100%)	74 (97%)	2 (3%)	41 60
51	U3	20/20 (100%)	19 (95%)	1 (5%)	20 42
51	U4	20/20 (100%)	20 (100%)	0	100 100
52	W4	50/50 (100%)	48 (96%)	2 (4%)	27 48
52	X3	50/50 (100%)	48 (96%)	2 (4%)	27 48
54	V3	101/101 (100%)	96 (95%)	5 (5%)	20 42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
54	V4	101/101 (100%)	98 (97%)	3 (3%)	36 56
All	All	9776/9776 (100%)	9535 (98%)	241 (2%)	43 62

5 of 241 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	U2	80	ARG
45	O4	64	ARG
36	F3	7	ASN
45	O4	17	ARG
52	W4	133	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
11	M2	31	HIS
36	F4	84	ASN
22	X2	70	GLN
35	E4	141	GLN
42	L4	76	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	A1	2911/2912 (99%)	1509 (51%)	28 (0%)
29	A2	2911/2912 (99%)	1483 (50%)	30 (1%)
30	B1	121/122 (99%)	62 (51%)	0
30	B2	121/122 (99%)	58 (47%)	1 (0%)
53	A3	1505/1506 (99%)	788 (52%)	26 (1%)
53	A4	1505/1506 (99%)	795 (52%)	16 (1%)
All	All	9074/9080 (99%)	4695 (51%)	101 (1%)

5 of 4695 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	A1	3	U
29	A1	4	C
29	A1	5	A
29	A1	6	A
29	A1	7	G

5 of 101 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	A2	2792	G
53	A3	670	A
53	A4	1305	A
53	A3	133	G
53	A3	382	U

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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	D3	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D3	10:ARG	C	11:LEU	N	4.44
1	D3	8:VAL	C	9:CYS	N	3.57

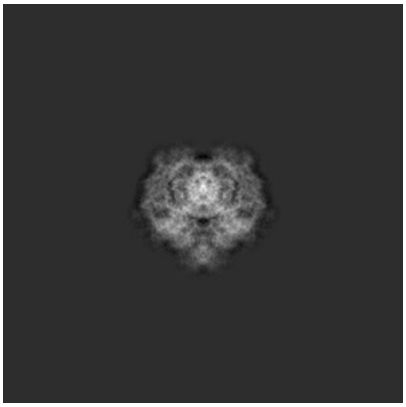
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-0104. These allow visual inspection of the internal detail of the map and identification of artifacts.

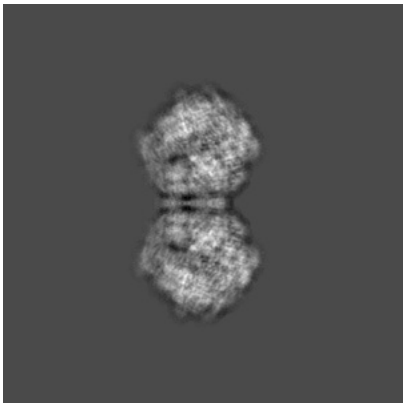
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

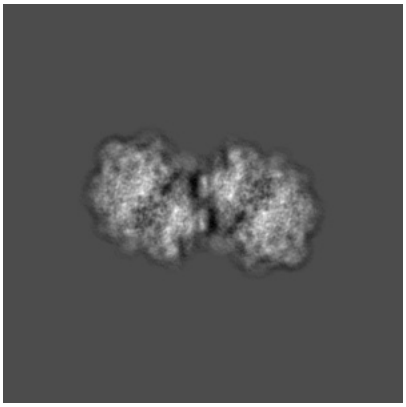
6.1.1 Primary map



X



Y



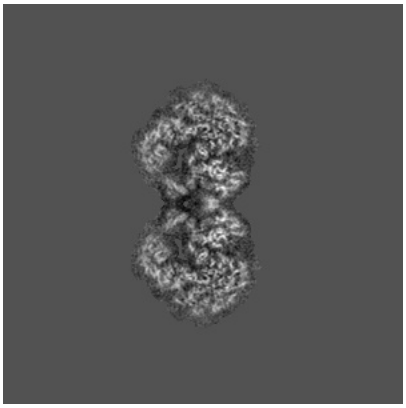
Z

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

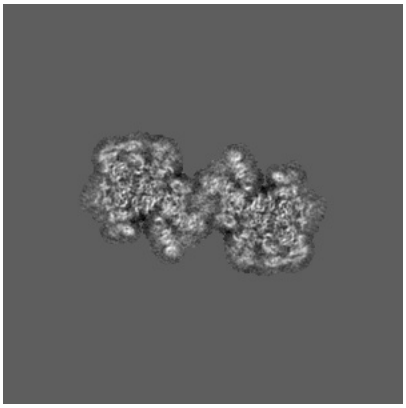
6.2 Central slices

6.2.1 Primary map

X Index: 350



Y Index: 350

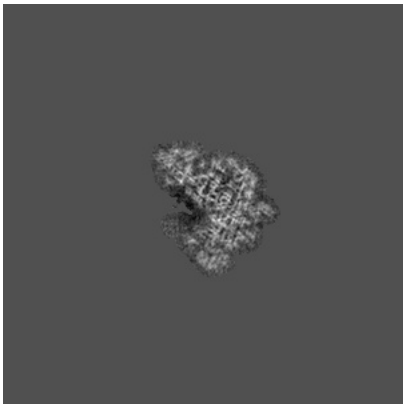


Z Index: 350

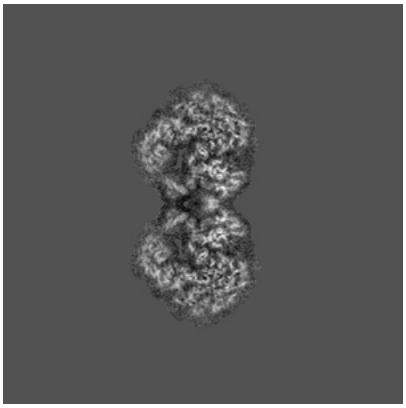
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

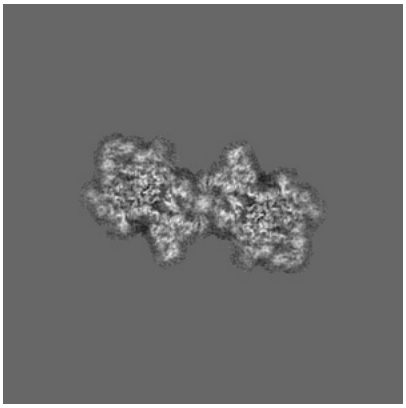
6.3.1 Primary map



X Index: 242



Y Index: 350

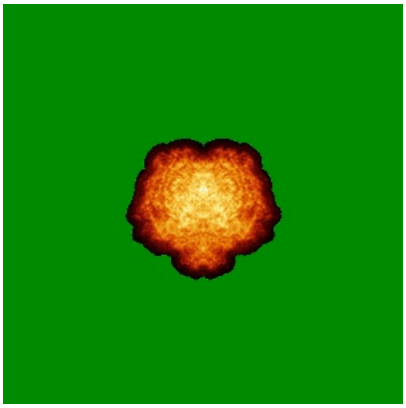


Z Index: 362

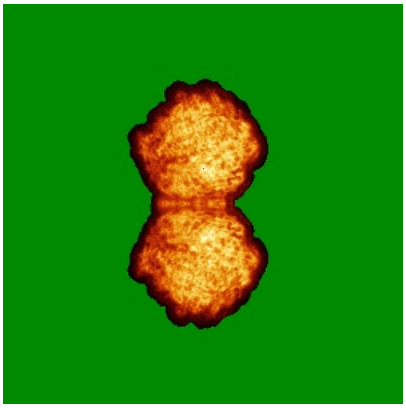
The images above show the largest variance slices of the map in three orthogonal directions.

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

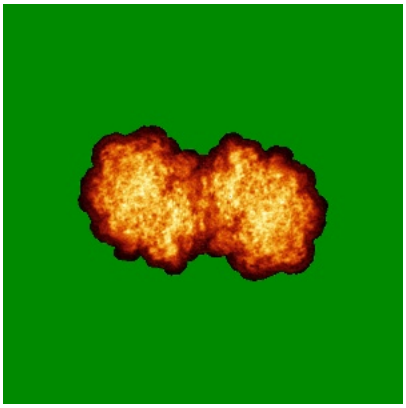
6.4.1 Primary map



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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 2.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

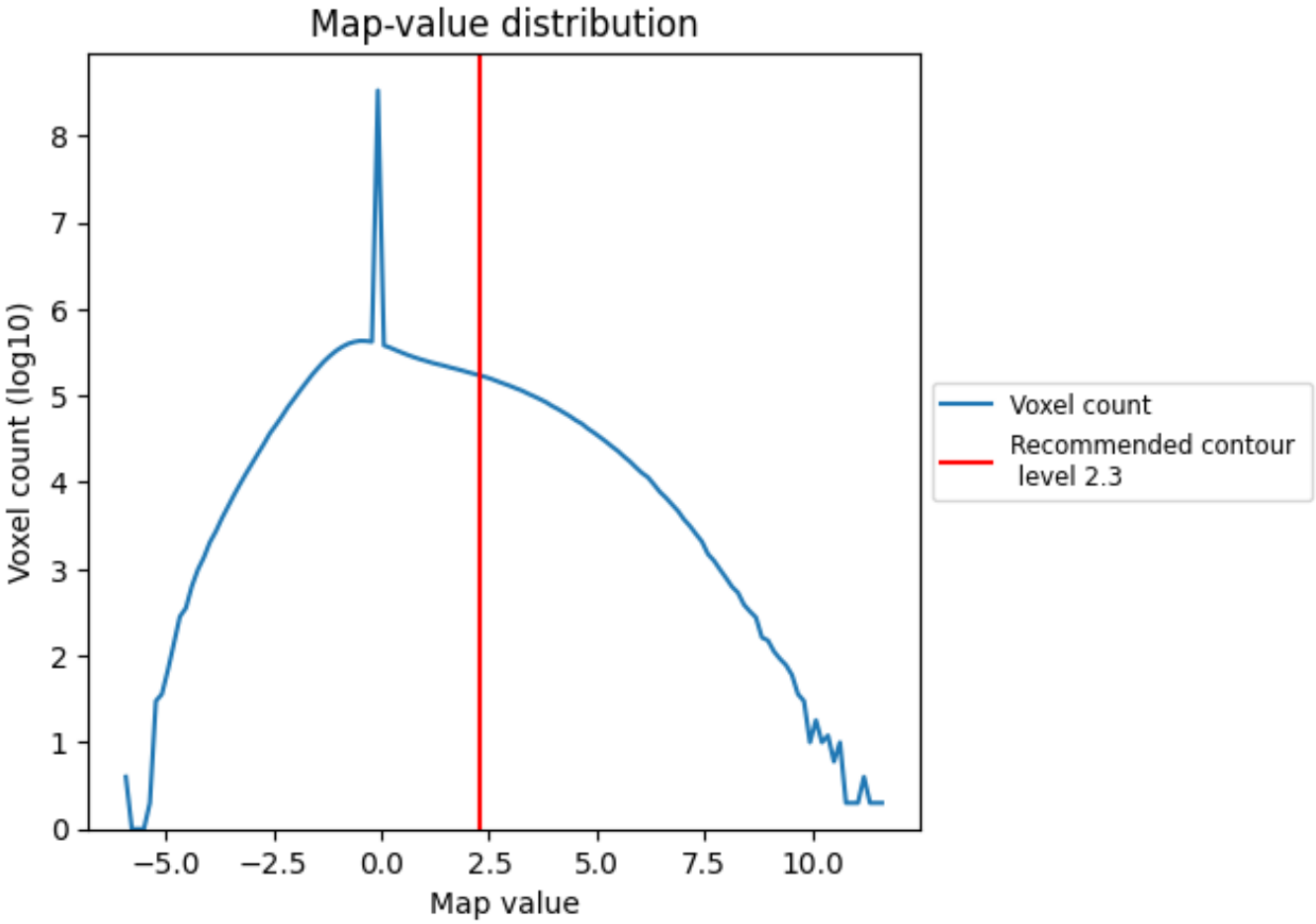
6.6 Mask visualisation (i)

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

7 Map analysis

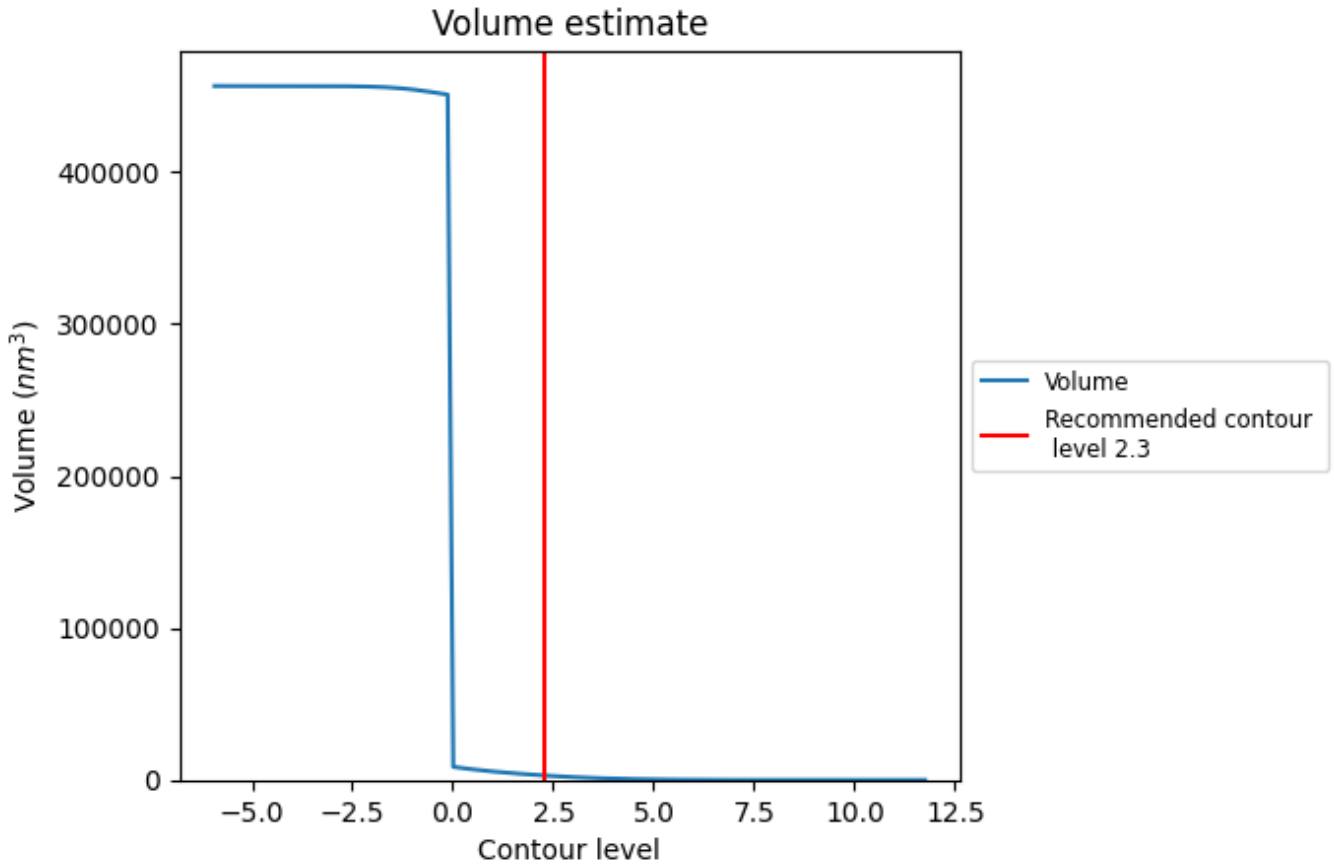
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

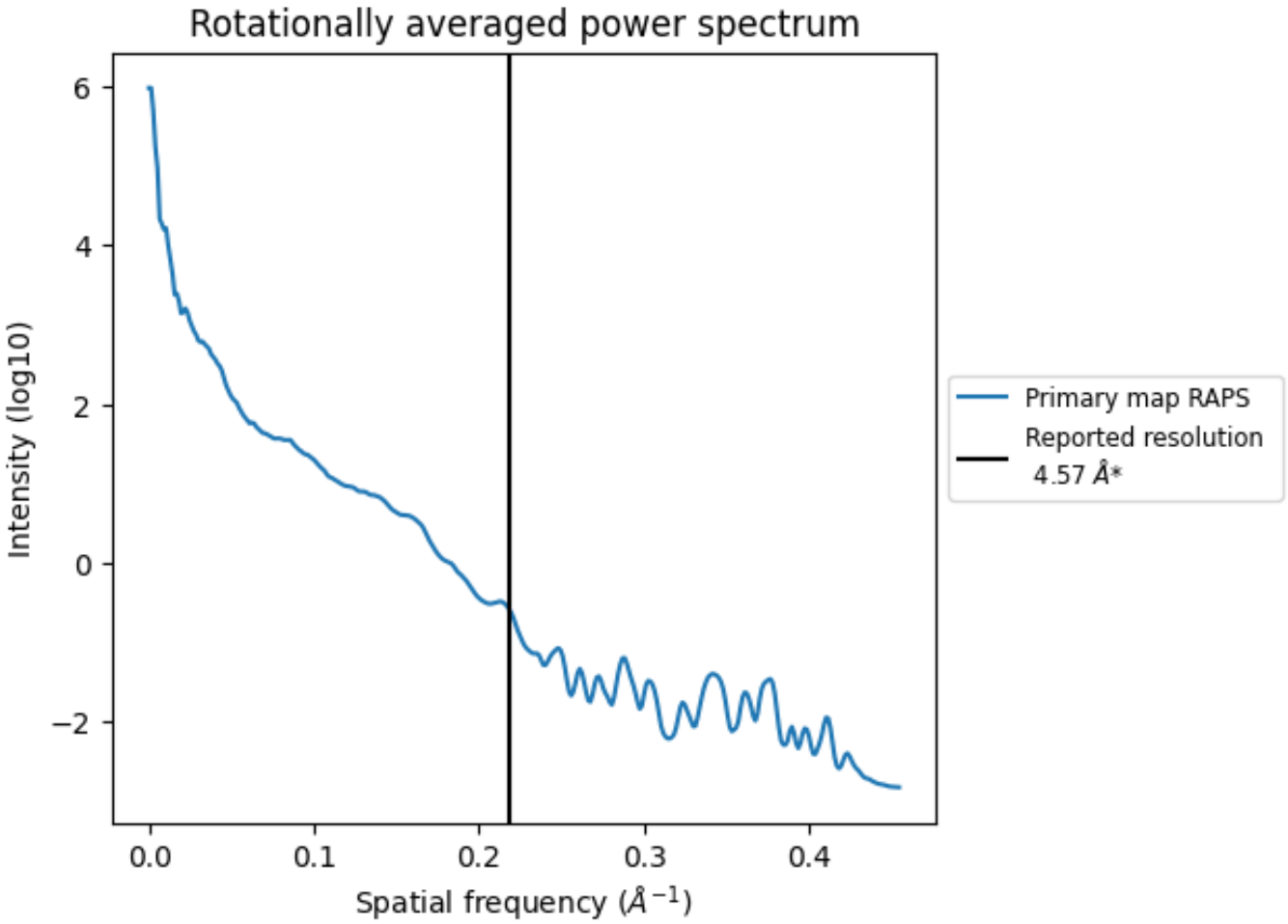
7.2 Volume estimate (i)



The volume at the recommended contour level is 2918 nm^3; this corresponds to an approximate mass of 2636 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.219 $Å^{-1}$

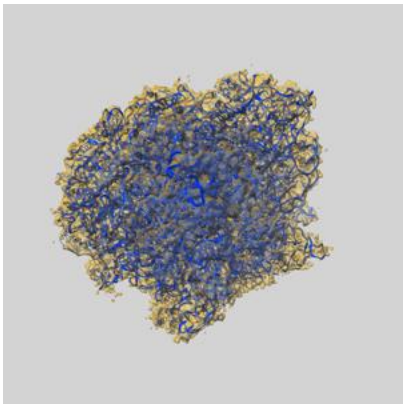
8 Fourier-Shell correlation (i)

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

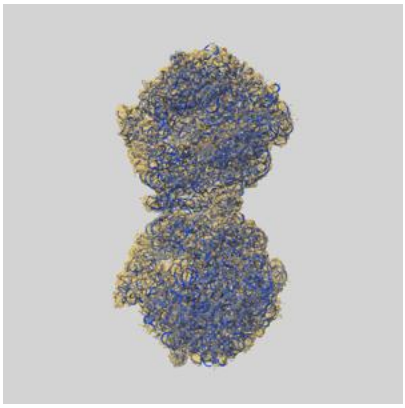
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-0104 and PDB model 6GZX. Per-residue inclusion information can be found in section 3 on page 18.

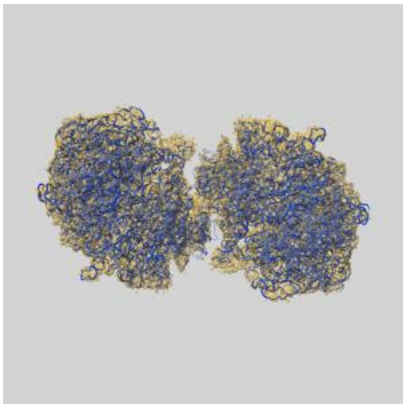
9.1 Map-model overlay



X



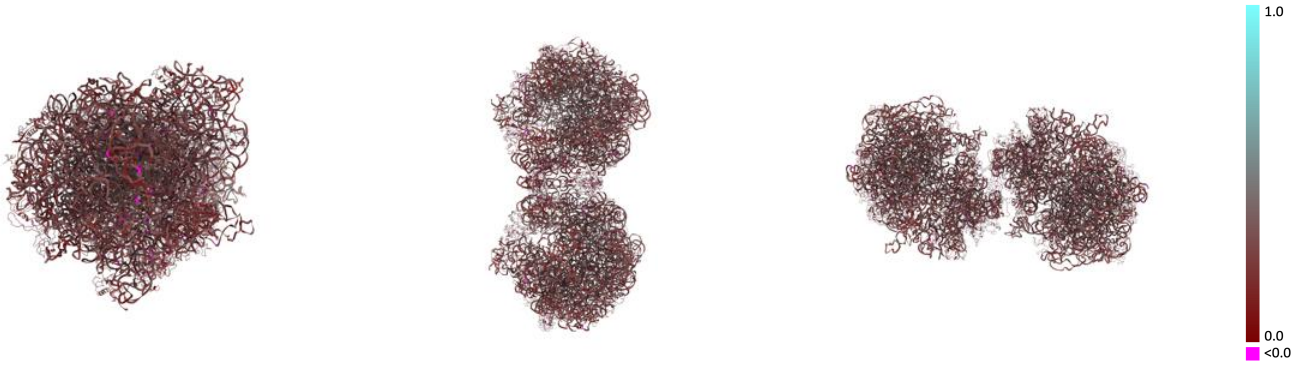
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.3 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.

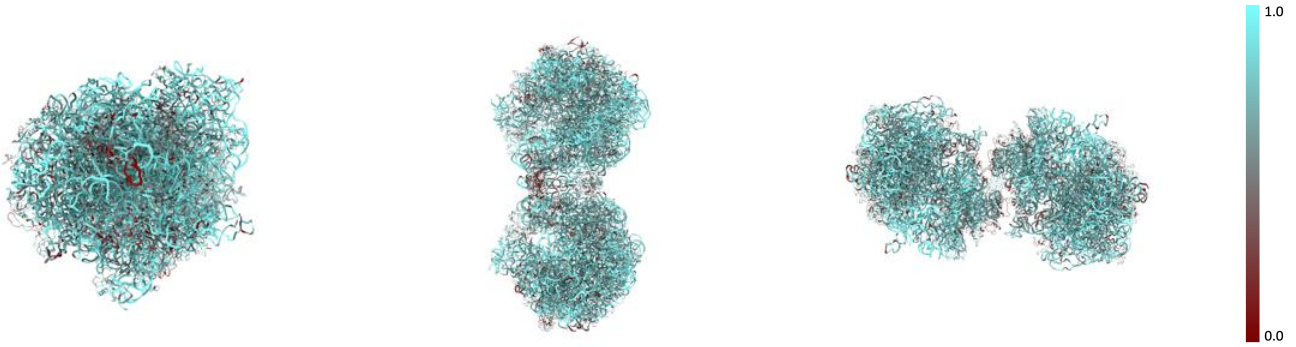
9.2 Q-score mapped to coordinate model



X Y Z

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

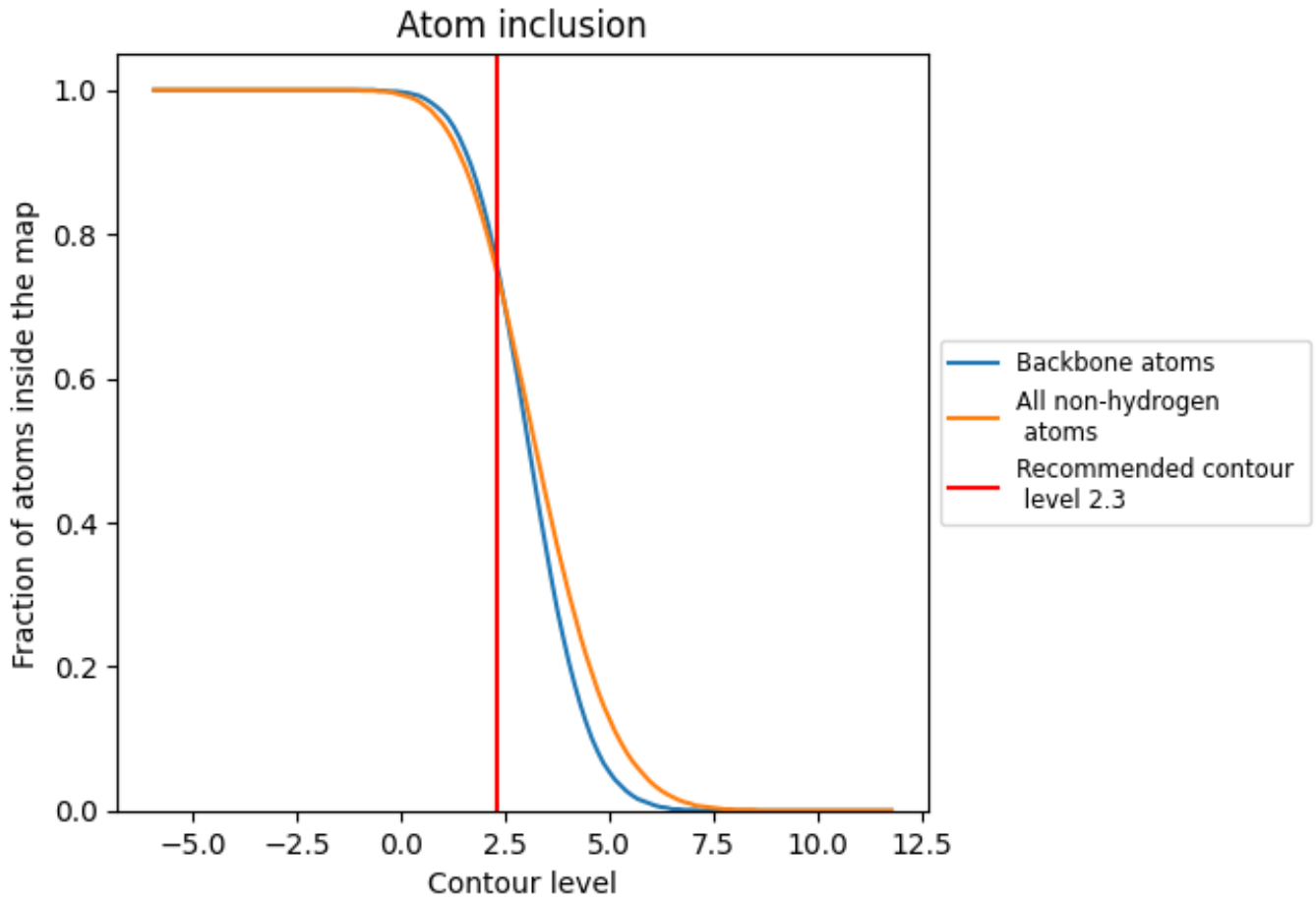
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.3).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 75% 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 (2.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7460	0.2820
A1	0.8230	0.2990
A2	0.8250	0.2990
A3	0.8550	0.2850
A4	0.8540	0.2860
B1	0.8790	0.2750
B2	0.8750	0.2760
B3	0.5860	0.2420
B4	0.5830	0.2420
C1	0.4360	0.2870
C2	0.4380	0.2860
C3	0.5890	0.2660
C4	0.5830	0.2630
D1	0.5050	0.2730
D2	0.5040	0.2750
D3	0.6900	0.2630
D4	0.7070	0.2690
E1	0.5560	0.2520
E2	0.5580	0.2580
E3	0.6330	0.2680
E4	0.6500	0.2620
F1	0.5790	0.2320
F2	0.5890	0.2290
F3	0.5300	0.2490
F4	0.5210	0.2570
G1	0.6190	0.2530
G2	0.5910	0.2480
G3	0.4570	0.2270
G4	0.4590	0.2270
H1	0.3490	0.2650
H2	0.3650	0.2590
H3	0.6330	0.2460
H4	0.6290	0.2450
I1	0.6230	0.2690
I2	0.6200	0.2780

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
I3	0.2530	0.2330
I4	0.2600	0.2390
J1	0.5510	0.2980
J2	0.5530	0.2920
J3	0.3690	0.2480
J4	0.3620	0.2500
K1	0.6190	0.2640
K2	0.6280	0.2620
K3	0.5670	0.2410
K4	0.5800	0.2380
L1	0.5800	0.2770
L2	0.5530	0.2670
L3	0.6270	0.2870
L4	0.6240	0.2910
M1	0.5900	0.2560
M2	0.5960	0.2510
M3	0.5770	0.2410
M4	0.5750	0.2180
N1	0.7050	0.2510
N2	0.7210	0.2280
N3	0.5550	0.2620
N4	0.5370	0.2520
O1	0.4980	0.2610
O2	0.5050	0.2590
O3	0.6410	0.2460
O4	0.6310	0.2580
P1	0.5440	0.2360
P2	0.5370	0.2490
P3	0.6170	0.2640
P4	0.6310	0.2500
Q1	0.4030	0.2710
Q2	0.3920	0.2880
Q3	0.5430	0.2730
Q4	0.5300	0.2810
R1	0.4910	0.2620
R2	0.4970	0.2530
R3	0.5910	0.2450
R4	0.5970	0.2440
S1	0.5540	0.2700
S2	0.5440	0.2660
S3	0.4440	0.2380
S4	0.5020	0.2200

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
T1	0.4300	0.2670
T2	0.4430	0.2660
T3	0.6560	0.2670
T4	0.6600	0.2630
U1	0.4160	0.2300
U2	0.4210	0.2370
U3	0.3580	0.2330
U4	0.3780	0.2370
V1	0.5680	0.2580
V2	0.5570	0.2580
V3	0.5830	0.2360
V4	0.5870	0.2420
W1	0.5360	0.2550
W2	0.5180	0.2580
W4	0.8070	0.2120
X1	0.6380	0.2670
X2	0.6680	0.2580
X3	0.7990	0.2120
Y1	0.3930	0.2650
Y2	0.3930	0.2680
Z1	0.6860	0.2450
Z2	0.6940	0.2510
a1	0.5710	0.2730
a2	0.5610	0.2640
b1	0.7730	0.2610
b2	0.7790	0.2590
c1	0.5400	0.2870
c2	0.5480	0.2890
d1	0.4640	0.2500
d2	0.4640	0.2400
e1	0.6400	0.2860
e2	0.6360	0.2770